



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 183912

TO: Ruixiang Li
Location: rem/4D59/4C70
Art Unit: 1646

April 6, 2006

Case Serial Number: 10/811198

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

78733
STIC-Biotech/ChemLib

183912

Mg

From: Li, Ruixiang
Sent: Saturday, April 01, 2006 9:34 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/811,198

Please do a standard search on:

SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D59
Mail Box 4C70
(571) 272-0875

RECEIVED
APR - 3 2006
STIC-BIOTECH/CHMLIB
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 20:07:07 ; Search time 233 Seconds
(without alignments)
1105.227 Million cell updates/sec

Title: US-10-811-198-2

Perfect score: 1944

Sequence: 1 MASTESSLLRLSLSPGPGS.....CRWAATPQDSGCTPRADRL 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	100.0	365	1	P2RY4_HUMAN
2	1944	100.0	365	2	P51582 homo sapien
3	1938	99.7	365	2	Q5J222 HUMAN
4	1935	99.5	365	2	Q502W2 HUMAN
5	1934	99.5	365	2	Q4VBB7 HUMAN
6	1597	82.2	361	1	Q4VBB8 HUMAN
7	1561	80.3	361	1	P2RY4_RAT
8	1176	60.5	230	2	P2RY4_MOUSE
9	1127.5	58.0	374	2	Q5Y809 sus scrofa
10	1038.5	53.4	347	2	Q57466 MELEAGRIS G
11	1022.5	52.6	543	2	Q7ZZA4 BRACHYDANIO
12	1007.5	51.8	537	1	Q5BJ79 XENTR
13	1007.5	51.8	537	2	P2RY8 XENLA
14	970.5	49.9	302	2	Q7ZM07 XENLA
15	965	49.6	377	1	Q4RP73 tetraodon n
16	962.5	49.5	373	1	P2RY2_HUMAN
17	950	48.9	374	1	P2RY2_MOUSE
18	940.5	48.4	373	2	P2RY2_RAT
19	910.5	46.8	349	2	Q5YA25 sus scrofa
20	823	42.3	165	1	P2RY4_CRICR
21	809	41.6	164	2	Q5DKX1 pig
22	803.5	41.3	310	2	Q4SEL5 TETNG
23	662	34.1	125	2	Q6QHU9 BOVIN
24	641.5	33.0	373	1	P2RY1_HUMAN
25	631	32.5	362	1	P2RY1_MELEGA
26	628	32.3	362	1	P2RY1_CHICK
27	628	32.3	373	1	P2RY1_CAVPO
28	621	31.9	373	1	P2RY1_BOVIN
29	620.5	31.9	357	2	Q9DE05 RAJER
30	616	31.7	373	1	P2RY1_RAT
31	614	31.6	373	1	P2RY1_MOUSE

32	614	31.6	373	2	Q544J5 MOUSE
33	611	31.4	373	2	Q5XX73 CANPA
34	611	31.4	373	2	Q8MX75 MOUSE
35	608.5	31.3	361	2	Q90X57 XENLA
36	607	31.2	308	2	Q4SEL9 TETNG
37	607	31.2	358	2	Q4SPQ4 TETNG
38	603	31.0	328	1	P2RY3_CHICK
39	599	30.8	328	1	P2RY3_MELEGA
40	592	30.5	328	2	Q5R5L6 PONPY
41	588	30.2	328	1	P2RY6_RAT
42	586	30.1	328	1	P2RY6_HUMAN
43	584	30.0	328	1	P2RY6_MOUSE
44	575	29.6	182	2	Q5DKX2 PIG
45	555	28.5	135	1	P2RY4_MERUN

ALIGNMENTS

RESULT 1

P2RY4_HUMAN					
ID	P2RY4_HUMAN	STANDARD;	PRT;	365 AA.	
AC	P51582;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	10-MAY-2005 (Rel. 47, Last annotation update)				
DE	P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).				
GN	Name=P2RY4; Synonyms=NRU;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=96125055; PubMed=8537336; DOI=10.1074/jbc.270.52.30849;				
RA	Communi D., Pirotton S., Parmentier M., Boeynaems J.-M.;				
RT	"Cloning and functional expression of a human uridine nucleotide				
RT	receptor.";				
RL	J. Biol. Chem. 270:30849-30852 (1995).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=96125054; PubMed=8537335; DOI=10.1074/jbc.270.52.30845;				
RA	Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,				
RA	Garrard R.C., George S.R., Turner J.T., O'Dowd B.F.;				
RT	"Cloning, expression, and chromosomal localization of the human				
RT	uridine nucleotide receptor gene.";				
RL	J. Biol. Chem. 270:30845-30848 (1995).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Pancreas;				
RX	MEDLINE=96197801; PubMed=8617367; DOI=10.1016/0014-5793(96)00321-3;				
RA	Stam N.J., Kloppe J., van der Heuvel M., Olfive W.;				
RT	"Molecular cloning and characterization of a novel orphan receptor				
RT	(P2P) expressed in human pancreas that shows high structural homology				
RT	to the P2U purinoceptor.";				
RL	FEBS Lett. 384:260-264 (1996).				
RN	[4]				
RP	PHOSPHORYLATION SITES SER-333 AND SER-334, AND MUTAGENESIS OF SER-243;				
RP	SER-333; SER-334 AND SER-339.				
RX	MEDLINE=21192241; PubMed=11114308; DOI=10.1074/jbc.M009909200;				
RA	Brinson A.E., Harden T.K.;				
RT	"Differential regulation of the uridine nucleotide-activated P2Y4 and				
RT	P2Y6 receptors. Ser-333 and Ser-334 in the carboxyl terminus are				
RT	involved in agonist-dependent phosphorylation desensitization and				
RT	internalization of the P2Y4 receptor.";				
RL	J. Biol. Chem. 276:11939-11948 (2001).				
CC	-1- FUNCTION: Receptor for UDP and UDP coupled to G-proteins that				
CC	activate a phosphatidylinositol-calcium second messenger system.				
CC	Not activated by ATP or ADP.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: Pancreas.				
CC	-1- PTM: Phosphorylation of Ser-333 and Ser-334 is a key step in				

Q544J5	m adult mal
Q5XX73	canis famil
Q8MX75	mus musculu
Q90X57	xenopus lae
Q4SEL9	tetraodon n
Q4SPQ4	tetraodon n
Q98907	gallus gall
Q93361	meleagris g
Q5R5L6	pongo pygma
Q63371	rattus norv
Q15077	homo sapien
Q9ERK9	mus musculu
Q5DKX2	sus scrofa
Q99PE4	meriones un

agonist-dependent desensitization and loss of surface P2RY4. This phosphorylation does not involve PKC, nor other calcium activated kinases.

1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; X91852; CAA62963.1; -; Genomic DNA.
EMBL; U40223; AAC50347.1; -; Genomic DNA.
EMBL; X96597; CAA65415.1; -; Genomic DNA.
PIR; S68679; S68679.
HSSP; P34996; 1DDD.
Ensembl; ENSG00000186912; Homo sapiens.
HGNC; HGNC:8542; P2RY4.
MIM; 300038; -.
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0015065; F: uridine nucleotide receptor activity; TAS.
GO; GO:0007204; P: positive regulation of cytosolic calcium io. . . ; TAS.
InterPro; IPR000276; GPCR_Rhodopsn.
InterPro; IPR002286; P2_purinoceptor.
InterPro; IPR000018; P2Y4_purinoceptor.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCR_Rhodopsn.
PRINTS; PR01066; P2Y4_Purinoceptor.
PRINTS; PR01157; P2Y4_Purinoceptor.
PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECPT_F1_2; 1.
Transducer; Transmembrane.
Transmembrane.
TOPO_DOM 1 34 Extracellular (Potential).
TRANSMEM 35 61 1 (Potential).
TOPO_DOM 62 72 Cytoplasmic (Potential).
TRANSMEM 73 95 2 (Potential).
TOPO_DOM 96 112 Extracellular (Potential).
TRANSMEM 113 131 3 (Potential).
TOPO_DOM 132 154 Cytoplasmic (Potential).
TRANSMEM 155 174 4 (Potential).
TOPO_DOM 175 196 Extracellular (Potential).
TRANSMEM 197 222 5 (Potential).
TOPO_DOM 223 246 Cytoplasmic (Potential).
TRANSMEM 247 269 6 (Potential).
TOPO_DOM 270 287 Extracellular (Potential).
TRANSMEM 288 309 7 (Potential).
TOPO_DOM 310 365 Cytoplasmic (Potential).
MOD_RES 333 333 Phosphoserine (Probable).
MOD_RES 334 334 Phosphoserine (Probable).
DISULFID 108 185 By similarity.
VARIANT 168 168 V -> M (in dbSNP:1152186).
VARIANT 178 178 /FTId=VAR_011854.
VARIANT 191 191 N -> T (in dbSNP:1152187).
VARIANT 191 191 /FTId=VAR_011855.
MUTAGEN 243 243 P -> L (in dbSNP:1152188).
MUTAGEN 333 365 /FTId=VAR_011856.
Missing: Abolishes agonist-induced phosphorylation. Prevents agonist-induced desensitization and loss of cell surface receptors.
SSALVSLPDSRCRWATPDSSCST->AALVALPEDA
ACRWAAQDAACAA: Greatly reduces agonist-induced desensitization and loss of cell surface receptors.
S->A: Greatly reduces agonist-induced desensitization and loss of cell surface receptors; when associated with A-334 and A-339.
S->A: Greatly reduces agonist-induced desensitization and loss of cell surface receptors; when associated with A-333 and

A-339.
S->A: Greatly reduces agonist-induced desensitization and loss of cell surface receptors; when associated with A-333 and A-334.
Missing: No effect on agonist-induced phosphorylation, no functional effect.
Missing: No functional effect.
L -> V (in Ref. 2).
S -> A (in Ref. 2).
Query Match 100.0%; Score 1944; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-131;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MASTESSLLRSLSGLSPGSGSEVELDCWDFDKFILLPVSVAVVFLVGLGNAPTLMLF 60
1 MASTESSLLRSLSGLSPGSGSEVELDCWDFDKFILLPVSVAVVFLVGLGNAPTLMLF 60

61 IPRLPWDATATYMFHLALSDTYLVSLPTLIYYAANHHWPGTEICKFVFLFYNNLY 120
61 IPRLPWDATATYMFHLALSDTYLVSLPTLIYYAANHHWPGTEICKFVFLFYNNLY 120

121 CSVLFLTCISVHYLIGICHLRALWRGRPRLAGLLCLAVLVVAGCLVPLNLFVTSNKG 180
121 CSVLFLTCISVHYLIGICHLRALWRGRPRLAGLLCLAVLVVAGCLVPLNLFVTSNKG 180

181 TTVLCHDITTRPEEFHYHFFSSAVNGLLFGVCLVTLVCYGLMARRLYPLPGSAQSSSR 240
181 TTVLCHDITTRPEEFHYHFFSSAVNGLLFGVCLVTLVCYGLMARRLYPLPGSAQSSSR 240

241 LRSLTIAVLTVFAVCFVPHITITTYLRLLEADCRVLTANVNVVYKVRPLASANSC 300
241 LRSLTIAVLTVFAVCFVPHITITTYLRLLEADCRVLTANVNVVYKVRPLASANSC 300

301 LDPVLYLLTGDKYRQLRQLCGGKPPQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
301 LDPVLYLLTGDKYRQLRQLCGGKPPQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360

361 RADRL 365
361 RADRL 365

RESULT 2
Q5JT22 HUMAN
ID Q5JT22_HUMAN PRELIMINARY; PRT; 365 AA.
AC Q5JT22_30 Created
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Pyrimidinergic receptor P2Y, G-protein coupled, 4 (Pyrimidinergic receptor P2Y4).
DE Name=P2RY4; ORFNames=RP13-26D14.5-001;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brown A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RC TISSUE=PCR rescued clones;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.F., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3]

NUCLEOTIDE SEQUENCE.

TISSUE=PCR rescued clones;

RG NIH MGC Project;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

DR EMBL; AL357752; CA14192.1; -; Genomic DNA.

DR EMBL; BC096070; AAH96070.1; -; mRNA.

DR EMBL; BC096067; AAH96067.1; -; mRNA.

DR Ensembl; ENSG00000186912; Homo sapiens.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signal. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR InterPro; IPR002286; P2_purnocptor.

DR InterPro; IPR000018; P2Y4_purnocptor.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PRINTS; PR01066; P2Y4_PNOCPTOR.

DR PRINTS; PR01157; P2Y4_PNOCPTOR.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SQ SEQUENCE 365 AA; 40963 MW; 23E0AFD3B7BDEED CRC64;

Query Match 100.0%; Score 1944; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-131;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVFVLGLGNAPTLLWF 60

DB 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVFVLGLGNAPTLLWF 60

QY 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKVRFPLFWNNLY 120

DB 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKVRFPLFWNNLY 120

QY 121 CSVLFTCTSVHRYLGICHLPRALRWGRPRLAGLCLAVLWLVAGCLVNLPRVTTNSKG 180

DB 121 CSVLFTCTSVHRYLGICHLPRALRWGRPRLAGLCLAVLWLVAGCLVNLPRVTTNSKG 180

QY 181 TTVLCHDTRTPPEFDHYHFFSVAMGLLFGVPCVLTVLCVGLMARLYQLPGSAQSSSR 240

DB 181 TTVLCHDTRTPPEFDHYHFFSVAMGLLFGVPCVLTVLCVGLMARLYQLPGSAQSSSR 240

QY 241 LRSRLTIAVLVTVFAVCFVFFHTRITRYILARLLEADCRVLNINVVYKVRPLASANSC 300

DB 241 LRSRLTIAVLVTVFAVCFVFFHTRITRYILARLLEADCRVLNINVVYKVRPLASANSC 300

QY 301 LDPVLYLLGDKYRRQLRQLCGGKQPPRTAASSLALVSLPDDSCRWATPDQSSCSTP 360

DB 301 LDPVLYLLGDKYRRQLRQLCGGKQPPRTAASSLALVSLPDDSCRWATPDQSSCSTP 360

QY 361 RADRL 365

DB 361 RADRL 365

RESULT 3

Q502W2 HUMAN

ID Q502W2 HUMAN PRELIMINARY; PRT; 365 AA.

AC Q502W2;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Pyrimidinergic receptor P2Y4.

GN Names=P2RY4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=G-protein coupled receptors;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=G-protein coupled receptors;

RG NIH MGC Project;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

DR EMBL; BC095503; AAH95503.1; -; mRNA.

DR Ensembl; ENSG00000186912; Homo sapiens.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR InterPro; IPR002286; P2_purnocptor.

DR InterPro; IPR000018; P2Y4_purnocptor.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PRINTS; PR01066; P2Y4_PNOCPTOR.

DR PRINTS; PR01157; P2Y4_PNOCPTOR.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SQ SEQUENCE 365 AA; 40950 MW; B400BA02C1742B02 CRC64;

Query Match 99.7%; Score 1938; DB 2; Length 365;

Best Local Similarity 99.7%; Pred. No. 2.9e-131;

Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVFVLGLGNAPTLLWF 60

DB 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVFVLGLGNAPTLLWF 60

QY 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKVRFPLFWNNLY 120

DB 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKVRFPLFWNNLY 120

QY 121 CSVLFTCTSVHRYLGICHLPRALRWGRPRLAGLCLAVLWLVAGCLVNLPRVTTNSKG 180

Db 121 CSVLFLTCISVHRYLGICHPRLALRWGRPRLAGLLCLAVMLVWAGCLVPLNLFVFTTSGK 180
Qy 181 TTVLCHDTRPEEDFHYVHFSSAVMGLLFGVPCLVTLVYCYGLMARRLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEDFHYVHFSSAVMGLLFGVPCLVTLVYCYGLMARRLYQPLPGSAQSSSR 240
Qy 241 LRSRTIAVLTAVFVCPVPHITRTIYYLARLLEADCRVLNINVVYKVRPLASANSC 300
Db 241 LRSRTIAVLTAVFVCPVPHITRTIYYLARLLEADCRVLNINVVYKVRPLASANSC 300
Qy 301 LDPVLYLLTGDKYRQLRQCGGKQPRTAASSLALVSLPDSRCRWAATPDQSSCSTP 360
Db 301 LDPVLYLLTGDKYRQLRQCGGKQPRTAASSLALVSLPDSRCRWAATPDQSSCSTP 360
Qy 361 RADRL 365
Db 361 RADRL 365

RESULT 4

Q4VBB7 HUMAN
ID Q4VBB7 HUMAN PRELIMINARY; PRT; 365 AA.
AC Q4VBB7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Pyrimidinergic receptor P2Y4.
GN Name=P2RY4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX NIH MGC Project;
RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL -1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL; BC096069; AAH96069.1; -; mRNA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR000018; P2Y4_purinocptor.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01066; P2Y4_Purinocptor.
DR PRINTS; PR01157; P2Y_Purinocptor.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 365 AA; 40953 MW; 7CE0AFED247EC2F1 CRC64;

Query Match 99.5%; Score 1935; DB 2; Length 365;
Best Local Similarity 99.5%; Pred. No. 4.7e-131;
Matches 363; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASTESLLSLSLGSLPGSGSEVELDCWFDKFKILLPVSYAVVFLGLNAPTLWLF 60
Db 1 MASTESLLSLSLGSLPGSGSEVELDCWFDKFKILLPVSYAVVFLGLNAPTLWLF 60
Qy 61 IFRLRPMDATATMYHLLALSDTLVLSLPTLIYYAAHNPFPCTEICKVRFIFYNNLY 120
Db 61 IFRLRPMDATATMYHLLALSDTLVLSLPTLIYYAAHNPFPCTEICKVRFIFYNNLY 120
Qy 121 CSVLFLTCISVHRYLGICHPRLALRWGRPRLAGLLCLAVMLVWAGCLVPLNLFVFTTSGK 180
Db 121 CSVLFLTCISVHRYLGICHPRLALRWGRPRLAGLLCLAVMLVWAGCLVPLNLFVFTTSGK 180
Qy 181 TTVLCHDTRPEEDFHYVHFSSAVMGLLFGVPCLVTLVYCYGLMARRLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEDFHYVHFSSAVMGLLFGVPCLVTLVYCYGLMARRLYQPLPGSAQSSSR 240
Qy 241 LRSRTIAVLTAVFVCPVPHITRTIYYLARLLEADCRVLNINVVYKVRPLASANSC 300
Db 241 LRSRTIAVLTAVFVCPVPHITRTIYYLARLLEADCRVLNINVVYKVRPLASANSC 300
Qy 301 LDPVLYLLTGDKYRQLRQCGGKQPRTAASSLALVSLPDSRCRWAATPDQSSCSTP 360
Db 301 LDPVLYLLTGDKYRQLRQCGGKQPRTAASSLALVSLPDSRCRWAATPDQSSCSTP 360
Qy 361 RADRL 365
Db 361 RADRL 365

RESULT 5

Q4VBB8 HUMAN
ID Q4VBB8 HUMAN PRELIMINARY; PRT; 365 AA.
AC Q4VBB8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Pyrimidinergic receptor P2Y4.
GN Name=P2RY4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

```

RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98421785; PubMed=97511165;
RG TISSUE=PCR rescued clones;
RT NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: BC096068, AAH96068.1; -, mRNA.
DR InterPro: IPR000276; GPCR Rhodopsin.
DR InterPro: IPR002286; P2_purinocptor.
DR Pfam: PF00001, 7tm 1, 1.
DR PRINTS: PR00237; GPCR Rhodopsin.
DR PRINTS: PR01066; P2Y4_PURNOCPTOR.
DR PRINTS: PR01157; P2Y_PURNOCPTOR.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G PROTEIN RECEPTOR FL_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 365 AA; 40947 MW; 68E0AFED3C0A19F1 CRC64;

Query Match 99.5%; Score 1934; DB 2; Length 365;
Best Local Similarity 99.7%; Pred. No. 5.6e-131;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60

QY 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYVYAAHNPFGTEICKFVFLFYNNLY 120
DB 61 IFLRPWDATATYMFHALSDTLVLSLPTLIYVYAAHNPFGTEICKFVFLFYNNLY 120

QY 121 CSVFLTCISVHYRIGICHPLRALRWGRPLAGLCLAVLWVAGCLVNLFFVTTNKG 180
DB 121 CSVFLTCISVHYRIGICHPLRALRWGRPLAGLCLAVLWVAGCLVNLFFVTTNKG 180

QY 181 TTVLCHDTRPEFHYHFFSAVWGLLGVCLVLCYGLMARLLVQLPGSQSSSR 240
DB 181 TTVLCHDTRPEFHYHFFSAVWGLLGVCLVLCYGLMARLLVQLPGSQSSSR 240

QY 241 LRSLEIAVLTVFAVCFVPPHITRTIYVLAARLLEADCKVLNVVYKVRPLASANS 300
DB 241 LRSLEIAVLTVFAVCFVPPHITRTIYVLAARLLEADCKVLNVVYKVRPLASANS 300

QY 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPDSSCRWAATPDSSCSTP 360
DB 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPDSSCRWAATPDSSCSTP 360

QY 361 RADRL 365
DB 361 RADRL 365

RESULT 6
ID P2RY4_RAT STANDARD; PRT; 361 AA.
AC O35811;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinoceptor 4 (P2Y4).
GN Name=P2Y4; Synonyms=P2Y4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=liver;
RA Bogdanov Y.D., Wildman S., King B.F., Burnstock G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

[2]
NUCLEOTIDE SEQUENCE.
STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=98421785; PubMed=97511165;
Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
"Molecular cloning and characterization of the rat P2Y4 receptor.";
J. Neurochem. 71:1348-1357(1998).
-1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that activate a phosphatidylinositol-calcium second messenger system.
-2- NOT ACTIVATED BY ADP OR UDP.
-3- SUBCELLULAR LOCATION: Integral membrane protein.
-4- TISSUE SPECIFICITY: Widely expressed at low levels. In brain, higher expression in the pineal gland and ventricular system.
-5- PTM: Phosphorylation of Ser-329 and Ser-330 is a key step in agonist-dependent desensitization and loss of surface P2RY4. This phosphorylation does not involve PKC, nor other calcium-activated kinases (By similarity).
-6- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL: Y14705; CAA75007.1; -; Genomic_DNA.
EMBL: Y11433; CAA72241.1; -; mRNA.
HSSP: P34996; 1DDD.
Ensembl: ENSRNOG000002953; Rattus norvegicus.
RGD: 61798; P2Y4.
GO: GO:0016324; C:apical plasma membrane; IDA.
GO: GO:00016323; F:basolateral plasma membrane; IDA.
GO: GO:0005524; F:ATP binding; IDA.
InterPro: IPR00276; GPCR Rhodopsin.
InterPro: IPR002286; P2_purinocptor.
InterPro: IPR000018; P2Y4_purinocptor.
Pfam: PF00001; 7tm 1, 1.
PRINTS: PR00237; GPCR Rhodopsin.
PRINTS: PR01066; P2Y_PURNOCPTOR.
PRINTS: PR01157; P2Y_PURNOCPTOR.
PROSITE: PS00237; G PROTEIN RECEPTOR FL_1; 1.
PROSITE: PS0262; G PROTEIN RECEPTOR FL_2; 1.
G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor; Transducer; Transmembrane.
TOPO_DOM 1 30 Extracellular (Potential).
TRANSMEM 31 58 1 (Potential).
TOPO_DOM 59 68 Cytoplasmic (Potential).
TRANSMEM 69 91 2 (Potential).
TOPO_DOM 92 108 Extracellular (Potential).
TRANSMEM 109 127 3 (Potential).
TOPO_DOM 128 149 Cytoplasmic (Potential).
TRANSMEM 150 170 4 (Potential).
TOPO_DOM 171 192 Extracellular (Potential).
TRANSMEM 193 218 5 (Potential).
TOPO_DOM 219 242 Cytoplasmic (Potential).
TRANSMEM 243 265 6 (Potential).
TOPO_DOM 266 283 Extracellular (Potential).
TRANSMEM 284 305 7 (Potential).
TOPO_DOM 306 361 Cytoplasmic (Potential).
MOD_RES 329 329 Phosphoserine (By similarity).
MOD_RES 330 330 Phosphoserine (By similarity).
CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).
DISULFID 104 181 By similarity.
SEQUENCE 361 AA; 40894 MW; 0377F96E54B449A3 CRC64;

Query Match 82.2%; Score 1597; DB 1; Length 361;
Best Local Similarity 82.7%; Pred. No. 9.1e-107;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
DB 1 MTSASLLFTSLGSPSGSGD-----DCRFNEFPILLPMSYAVVFLGLGNAPTLMWF 56

```

[illegible]

• RESULT 7

AC	Q9JUS7;	STANDARD;	PRT;	361 AA.
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	P2Y purinoceptor 4 (P2Y4);			
GN	Name=P2Y4; Synonyms=P2Y4r;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=129/SVJ;			
RC	MEDLINE=21185993; PubMed=11290369; DOI=10.1016/S0014-2999(01)00875-5;			
RA	Suarez-Huerta N., Pouillon V., Boeynaems J.-M., Robaye B.;			
RT	"Molecular cloning and characterization of the mouse P2Y4 nucleotide receptor.";			
RL	Eur. J. Pharmacol. 416:197-202(2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MENA].			
RC	STRAIN=C57BL/6J; TISSUE=Skin;			
RC	MEDLINE=2354693; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Naito I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Seisel K.W.,			
RA	Blake J.A., Bratt D., Brusuc V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,			
RA	Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,			
RA	Sulciana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,			
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,			
RA	Shizaki T., Waki J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,			


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QY 61 IFRLRPMDATATYMFHLALSDTLVLSLPTLLIYAAAHNHPFGTEICKFVRFELFYNNLY 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 LFRLRPMDATATYMFHLALSDTLVLSLPTLLIYAAAHNHPFGTEICKFVRFELFYNNLY 116
QY 121 CSVLFLTCISVHRVYIGICHPRLALRWGRPRAGLLCLAVLWVAGCLVPLNFFVTTNKG 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 CSVLFLTCISVHRVYIGICHPRLALRWGRPRAGLLCLAVLWVAGCLVPLNFFVTTNKG 176
QY 181 TTVLCHDTRPEEDHYHFSAVNGLLFGVPCVLTIVLCYGLMARRLYQPLPGSAQSSR 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
177 TTVLCHDTRPEEDHYHFSAVNGLLFGVPCVLTIVLCYGLMARRLYQPLPGSAQSSR 236
QY 241 LRSRLTIAVLTVFAVCFVPHIIRTYIYLARLLEADCRVLNIVNVVKKVTRPLASANS 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 LRSRLTIAVLTVFAVCFVPHIIRTYIYLARLLEADCRVLNIVNVVKKVTRPLASANS 296
QY 301 LDPVLYLTGKYRQLRQLCGGKQPORPTAASSIALVSLPDSSCRWAATPODSSCTP 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 LDPVLYLTGKYRQLRQLCGGKQPORPTAASSIALVSLPDSSCRWAATPODSSCTP 356
QY 361 RADRL 365
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 EGDRL 361

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RESULT 8

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QY Q5Y809_PIG PRELIMINARY; PRT; 230 AA.
AC Q5Y809;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE P2Y4 nucleotide receptor (fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15280443; DOI=10.1126/mol.104.002642;
RA Shen J., Seve C.I., Wang M., Weisman G.A., Wilden P.A., Sturek M.;
RT "Cloning, Up-Regulation, and Mitogenic Role of Porcine P2Y2 Receptor
in Coronary Artery Smooth Muscle Cells."
RL Mol. Pharmacol. 66:1265-1274(2004).
DR EMBL; AY662405; AAU89437.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR000018; P2Y4_purinocptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01066; P2Y4PRNOCPT.
DR PRINTS; PR01157; P2YPRNOCPT.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 230 230
SQ SEQUENCE 230 AA; 26199 MW; 2EADDF1BF18C49B9 CRC64;

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Query Match 60.58; Score 1176; DB 2; Length 230;
Best Local Similarity 92.24; Pred. No. 1.1e-76;
Matches 212; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 29 FDEDFKILLPVSVAVVVLGLGNAPTLWLFIRLRPMDATATYMFHLALSDTLVLSL 88
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 FDEDFKILLPVSVAVVVLGLGNAPTLWLFIRLRPMDATATYMFHLALSDTLVLSL 60

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QY 89 PTLIYAAAHNHPFGTEICKFVRFELFYNNLYCSVLFLTCISVHRVYIGICHPRLALRWGR 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 PTLIYAAAHNHPFGTEICKFVRFELFYNNLYCSVLFLTCISVHRVYIGICHPRLALRWGR 120
QY 149 PRLAGLLCLAVLWVAGCLVPLNFFVTTNKGTTVLCHDTRPEEDHYHFSAVNGLL 208
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 PRASLLCLAVLWVAGCLVPLNFFVTTNKGTTVLCHDTRPEEDHYHFSAVNGLL 180
QY 209 FGVPCLVTVLCYGLMARRLYQPLPGSAQSSRLRSLRTIAVLTVFAVCF 258
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 FGVPCLVTVLCYGLMARRLYQPLPGSAQSSRLRSLRTIAVLTVFAVCF 230

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RESULT 9

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QY Q57466_MELGA PRELIMINARY; PRT; 374 AA.
AC Q57466;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE G protein coupled P2Y nucleotide receptor.
GN Name=tp2Y;
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=98086419; PubMed=9415702;
RA Boyer J.L., Waldo G.L., Harden T.K.;
RT "Molecular cloning and expression of an avian G protein-coupled P2Y
receptor."
RL Mol. Pharmacol. 52:928-934(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AF031897; AAC60339.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000226; GPCR_Rhodops.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR000018; P2Y4_purinocptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01066; P2Y4PRNOCPT.
DR PRINTS; PR01157; P2YPRNOCPT.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 374 AA; 42594 MW; 849C465722BDD02B CRC64;

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Query Match 58.08; Score 1127.5; DB 2; Length 374;
Best Local Similarity 59.34; Pred. No. 5.2e-73;
Matches 208; Conservative 56; Mismatches 70; Indels 17; Gaps 4;
QY 9 LRSGLSP-----GPGSSEVLDQWDEKFKILLPVSVAVVVLGLGNAPTLW 58
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 VRMSLAPWTPPTPWLGGNTTAAAKCVNFBEKFPILLPISYGVVVGVLPLNSWAMW 64
QY 59 LFIIRLRPMDATATYMFHLALSDTLVLSLPTLLIYAAAHNHPFGTEICKFVRFELFYNN 118
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 IFVSRMEPNWNTTYMFLALSDTLVLSLPTLLIYAAAHNHPFGTEICKFVRFELFYNN 124
QY 119 LYSVFLTCISVHRVYIGICHPRLALRWGRPRAGLLCLAVLWVAGCLVPLNFFVTTN 178
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 LYSSILFLTCISVHRVYIGICHPRLALRWGRPRAGLLCLAVLWVAGCLVPLNFFVTTN 184
QY 179 KGTTVLCHDTRPEEDHYHFSAVNGLLFGVPCVLTIVLCYGLMARRLYQ---PLPGSA 235
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 185 KDNSTLCHDTTPKEFDHYHYSSIMALLFGIFPLVIVVYCYLMAKELCKSPSPSPR 244
Qy 236 QSSRLRLRTIAVLTAVFVAVCFVPHFTHRTIYILARLLEADCRVLINVVVYKTRPLA 295
Db 245 VPSYKGRSIIKIIIVLTFAICFVPHFTHRTIYILARLLEADCRVLINVVVYKTRPLA 304
Qy 296 SANSCLDPVLVLLGDKYRRQLQCGGKQPRTAASS-LALVSLPDDSS 345
Db 305 SINSCLDPILYFMAGDKYGRLLR---GAAQRPVPTSLALVSPVSDSS 352
RESULT 10
Q7ZZN4 BRARE PRELIMINARY; PRT; 347 AA.
AC Q7ZZN4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Novel protein similar to nucleotide receptors
GN Name=pr2y41; Synonyms=OTDARPO0000001909; ORFNames=bz46j2.9-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Skuce C.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AL590151; CAD68067.1; -; Genomic_DNA.
DR ZFIN; ZDB-GENE-030616-77; pr2y41.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purnocptor.
DR InterPro; IPR000018; P2y4_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01066; P2y4PRNOCPTR.
DR PRINTS; PR01157; P2YPRNOCPTR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; UNKNOWN 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
DR KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F83CC283E2 CRC64;
Query Match 53.4%; Score 1038.5; DB 2; Length 347;
Best Local Similarity 61.2%; Pred. No. 1.2e-66;
Matches 196; Conservative 39; Mismatches 82; Indels 3; Gaps 1;
Qy 20 SSEVELDCWFEDKFKILLPVSAYVFLVGLGNAPTLLWFLRPLPNDATATVYFHIAL 79
Db 5 SKEVNFSTDEEFYKILLPVSYSYVFLGLTINSLVALWMTKKRPWKPSTVYFHIAL 64
Qy 80 SDTLVLSLPTLIYYAAHNHPFTEICKFVFLYWNLYCSVFLFTICISVHYRLGICH 139
Db 65 SDTLVLSLPLIYYANRSHWPGVVLCKIVRFLFYANLYCSILFLTICISVHYRLGICH 124
Qy 140 PLRLRWGRPLRGLGLLAVLVAGLVVNLFFVTTNKGKTVLCHDTTPPEEDHYVH 199
Db 125 FIRSLTIKPRAHMVCVGFVMTAVIACLVPTLILVNTSRNGNSTLCHDTSRPEEFHFT 184
Qy 200 FSSAVNGLLFGVPLVTLVLCYGLMARLYQPLPGSA---QSSRLRLRTIAVLTAVF 256
Db 185 YNSVVMVLLFPLFVIVVYCYLMARALCQPRKGLAQNQSSSRKSKSLIIVLVVFAI 244
Qy 257 CFVPHFTHRTIYILARLLEADCRVLINVVVYKTRPLASNSCLDPVLVLLTGKYRQ 316
Db 245 CFVPHFTHRTIYILARLLEADCRVLINVVVYKTRPLASNSCLDPILYFLAGDHYRSK 304

Qy 317 LRQLCGGKQPRTAASSLA 336
Db 305 LLRLVTRQTNTSTRSTAYEYA 324

RESULT 11

Q5BJ79_XENTR PRELIMINARY; PRT; 543 AA.
AC Q5BJ79;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUS=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA TISSUS=Embryo;
RC Klein S., Gerhard D.S.;
RX Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL; BC091589; AAH91589.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purnocptor.
DR InterPro; IPR000018; P2y4_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01066; P2y4PRNOCPTR.
DR PRINTS; PR01157; P2YPRNOCPTR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; UNKNOWN 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
DR KW G-protein coupled receptor; Hypothetical protein; Receptor;
SQ Transducer; Transmembrane.
SEQUENCE 543 AA; 62234 MW; 23BD2FD005C3B901 CRC64;

Query Match 52.6%; Score 1022.5; DB 2; Length 543;
Best Local Similarity 53.7%; Pred. No. 2.5e-65;
Matches 196; Conservative 54; Mismatches 94; Indels 21; Gaps 5;

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QY 1 MASTESSLRSLRSLGSPGSSSEVLDQWDEKELLPSVAVVFLGLGNAPTLWLF 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 MATLHPSLLTTLPL-PKNLTNNTEDSCVFNKGKELLPLPISGVFMVGLPLNITAIWIF 64
QY 61 IFLRLPWPATATYMHLLALSDTLVLSLPTLLIYYAAHNPFGTEICKFVRFLFYWNLY 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 IAKRPPWNPPTTYMFLNALSDTLVLSLPTLLIYYAADQNNWPFVALCKIVRFLFYANLY 124
QY 121 CSVLPLTCISVHRHYGICHPLRALRWGRPRAGLLCLAVLWVAGCLVNPFLFFVTSNKG 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 SSILPLTCISVHRHYGVGCHPTTLTCLMAKHAHVICALVLSVMLCLVNPFLMEVTVSPKV 184
QY 181 TTVLCHDTRPEEFHYHFFSSAVMGLFGVPLVTLVCYGLMARLLYQPL-PGSAQS-- 237
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 NGTICHDTLPEEFKDYVEYSTGIMCLLFGIPCLIIACCYGLMARELMKPLVNGHQTLP 244
QY 238 SSRSLRLTIAVLTVFVAVCPVPHITRTIYYLARLEADCRVLNVVYKVRPLASA 297
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
245 SYKRSIKTIIVIVIAFAICFMPFHITRTIYYARLLGVNCYALNVINFTYKTRPLASA 304
QY 298 NSCLDPVLYLTGDKYRQL-----RQLC-----GGKPKQPTRAASSIALVSL 340
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 NSCIDPLIYFLANDRYRRLLRTVRRSVHRRCMHTNHPGHPPEPHMTTGPLPVVSA 364
QY 341 PEDSS 345
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
365 EETQS 369
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RESULT 12
ID P2Y8 XENLA STANDARD; PRT; 537 AA.
AC P79925;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinocceptor 8 (P2Y8).
OS Name=P2Y8;
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Neural plate;
RX MEDLINE=97284734; PubMed=9139711; DOI=10.1074/jbc.272.19.12583;
RA Bogdanov Y.D., Dale L., King B.F., Whittock N., Burnstock G.;
RT "Early expression of a novel nucleotide receptor in the neural plate
of Xenopus embryos";
RL J. Biol. Chem. 272:12583-12590 (1997).
CC -!- FUNCTION: Receptor for extracellular ATP, UTP, CTP, GTP and ITP.
CC The activity of this receptor is mediated by G proteins which
CC activate a phosphatidylinositol-calcium second messenger system.
CC May play a key role in the early development of neural tissue.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X99953; CAA68213.1; -; mRNA.
CC HSSP; P34996; 1DDD.
CC InterPro; IPR000276; GPCR_Rhodopn.
CC InterPro; IPR002286; P2Y_purinocptor.
CC InterPro; IPR000018; P2Y4_purinocptor.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01066; P2Y4PRNOCPTR.
CC PRINTS; PR01157; P2YPRNOCPTR.
```

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DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 49 Extracellular (Potential).
FT TRANSMEM 50 70 1 (Potential).
FT TOPO_DOM 71 79 Cytoplasmic (Potential).
FT TRANSMEM 80 100 2 (Potential).
FT TOPO_DOM 101 118 Extracellular (Potential).
FT TRANSMEM 119 139 3 (Potential).
FT TOPO_DOM 140 161 Cytoplasmic (Potential).
FT TRANSMEM 162 182 4 (Potential).
FT TOPO_DOM 183 210 Extracellular (Potential).
FT TRANSMEM 211 231 5 (Potential).
FT TOPO_DOM 232 254 Cytoplasmic (Potential).
FT TRANSMEM 255 275 6 (Potential).
FT TOPO_DOM 276 292 Extracellular (Potential).
FT TRANSMEM 293 316 7 (Potential).
FT TOPO_DOM 317 537 Cytoplasmic (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT DISULFID 116 193 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 537 AA; 62024 MW; B2CF24812F3C19F2 CRC64;
Query Match 51.8%; Score 1007.5; DB 1; Length 537;
Best Local Similarity 55.9%; Pred. No. 36-64;
Matches 190; Conservative 50; Mismatches 83; Indels 17; Gaps 4;
QY 20 SSVELDCWFDKFKILLPVSVAVFLGLGNAPTLWLFIFRLRPWDATATYMHFLAL 79
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 TNDTDCVDEGFKELLPVSVAVFLGLGNAPTLWLFIFRLRPWDATATYMHFLAL 87
QY 80 SDTLVLSLPTLLIYYAAHNPFGTEICKFVRFLFYWNLYCVSLFVLTCTSVHRYLGICH 139
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
88 SDTLVLSLPTLLIYYAADQNNWPFVALCKIVRFLFYANLYSSILFVLTCTSVHRYGVCH 147
QY 140 PLEALRWGRPRAGLLCLAVLWVAGCLVNPFLFFVTSNKGKPKQPTRAASSIALVSL 199
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
148 PITSLRRMAKHAHVICALVLSVMLCLVNPFLMEVTVSPKVPHTTGTTPEDFARYVE 207
QY 200 FSSAVMGLFGVPLVTLVCYGLMARLLYQPL-PGSAQS--SSRLSLRLTIAVLTVFVAV 256
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208 YSTAINCLLFGIPCLIIACCYGLMARELMKPLVNGHQTLPYKRSIKTIIVIAFAI 267
QY 257 CFVPHITRTIYYLARLEADCRVLNVVYKVRPLASANSCLDPVLYLTGDKYRQ 316
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
268 CFVPHITRTIYYARLLGVNCYALNVINFTYKTRPLASANSCLDPVLYLTGDKYRQ 327
QY 317 L-----RQLCGGKPKQ--PRTAASSIALVSLPE 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
328 LIKTVRRSSVNPNNRCMHTNHPGHPPEPHMTTGPLPVISAE 367
RESULT 13
Q7ZKQ7 XENLA PRELIMINARY; PRT; 537 AA.
AC Q7ZKQ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P2ry4-prov protein.
GN Name=p2ry4-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```


QY 140 PLRALRWGPRLAGLCLLAWLWVAGCLVPLNFFVTTTSKGTIVLCHDTRRBEEDHYH 199
 Db 120 PIKALNLVPRHSYLVCAWVAVVCLVPLNFFVTTTSKGTIVLCHDTRRBEEDHYH 179
 QY 200 FSSAVMGLLFGVPCVTLVLCYGLMARRLYQPLFGSAQ----SSRLRLSRLTIAVLTIFA 255
 Db 180 YCSVVMVFLFGVPLVIVVYCYCLMARTLCRPRVGLSSROGAVSYQKTLKLIIMVLMFA 239
 QY 256 VCFVPHTRTYIYLLARLEADCRVLNINVVYKVRPLASANSCLDPVLYLLTGDKYR 315
 Db 240 MCFVPHTRTYIYLLARLEADCRVLNINVVYKVRPLASANSCLDPVLYLLTGDKYR 315
 QY 316 QL 317
 Db 300 RL 301

RESULT 15

P2RY2 HUMAN
 ID P2RY2 HUMAN STANDARD; PRT; 377 AA.
 AC P41231; Q96EM8;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
 DN (Purinoceptor receptor)
 GN Name=P2RY2; Synonyms=P2R1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Airway epithelium;
 RX MEDLINE=94211846; PubMed=8159738;
 RA Parr C.E., Sullivan D.M., Faridiso A.M., Lazarowski E.R., Burch L.H.,
 Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
 "Cloning and expression of a human P2U nucleotide receptor, a target
 for cystic fibrosis pharmacotherapy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3275-3279 (1994).
 RN [2]
 RP SEQUENCE REVISION.
 RX MEDLINE=95108098; PubMed=7809171;
 RA Parr C.E., Sullivan D.M., Faridiso A.M., Lazarowski E.R., Burch L.H.,
 Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
 "Cloning and expression of a human P2U nucleotide receptor, a target
 for cystic fibrosis pharmacotherapy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:13067-13067 (1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RA Publ H.L. III, Ikeda S.R., Aronstam R.S.;
 "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guchrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney, and Leukocyte;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 activate a phosphatidylinositol-calcium second messenger system.
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
 CC = ADP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and
 CC brain.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U07225; AAC04923.1; -; mRNA.
 DR EMBL; AY136753; AA001279.1; -; mRNA.
 DR EMBL; BC012104; AA012104.1; -; mRNA.
 DR EMBL; BC028135; AA028135.1; -; mRNA.
 DR HSSP; P34996; 1DD0.
 DR Ensembl; ENSG00000175591; Homo sapiens.
 DR HGNC; HGNC:8541; P2RY2.
 DR H-InvDB; HIX0009916; -.
 DR MIM; 600041; -.
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004872; F: receptor activity; TAS.
 DR GO; GO:0006873; P: cell ion homeostasis; TAS.
 DR GO; GO:0007200; P: G-protein signaling, coupled to IP3 second . . . ; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR002286; P2_purinocptor.
 DR InterPro; IPR000356; P2U_purinocptor.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR00594; P2Y2_P2RY2.
 DR PRINTS; PR01157; P2Y_P2RY2.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02623; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 Transmembrane.
 FT TOPO_DOM 1 32 Extracellular (Potential).
 FT TRANSMEM 33 59 1 (Potential).
 FT TOPO_DOM 60 70 Cytoplasmic (Potential).
 FT TRANSMEM 71 93 2 (Potential).
 FT TOPO_DOM 94 110 Extracellular (Potential).
 FT TRANSMEM 111 129 3 (Potential).
 FT TOPO_DOM 130 152 Cytoplasmic (Potential).
 FT TRANSMEM 153 172 4 (Potential).
 FT TOPO_DOM 173 194 Extracellular (Potential).
 FT TRANSMEM 195 220 5 (Potential).
 FT TOPO_DOM 221 246 Cytoplasmic (Potential).
 FT TRANSMEM 247 269 6 (Potential).
 FT TOPO_DOM 270 287 Extracellular (Potential).
 FT TRANSMEM 288 309 7 (Potential).
 FT TOPO_DOM 310 377 Cytoplasmic (Potential).
 FT CARBOHYD 9 9 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc . .) (Potential).
 FT DISULFID 106 183 By similarity.
 FT CONFLICT 312 312 R -> S (in Ref. 4; AA012104).
 FT CONFLICT 350 350 E -> G (in Ref. 1).
 FT CONFLICT 359 359 S -> F (in Ref. 1).
 SQ SEQUENCE 377 AA; 42290 MW; EE557A857A269AC6 CRC64;

Query Match 49.6%; Score 965; DB 1; Length 377;
 Best Local Similarity 59.1%; Pred. No. 2.5e-61;
 Matches 185; Conservative 40; Mismatches 86; Indels 2; Gaps 1;

Qy	22	EVELDCWFDEDFKFIILLPVSYAVVFLGGLGINAPTLMLFIERLRPMDATATYMFHLALSD	81
Db	20	ELGYRCFNEDEKXVLLPVSYGVVGLGCLNAVALYIFLCRLKTNWASTTYMFHLAVSD	79
Qy	82	TLXVLSLPTLIYYIAAHNHPFGTEICKFVRFLFYNNLYCSVLFLTCISVHRYLIGICHPL	141
Db	80	ALYAASLPLLVYYIYARGDHPFSTVLCVRLFYTNLYCSILFLTCISVHRCLGVLRLPL	139
Qy	142	RALRWGPRLAGLLCLAVLWVAGCLVPLNFVVTTSNKGTTVLCHDTRPEEFDHYVHFS	201
Db	140	RSURWGRARVARRVAGAVWVLVLAQAPVLYFVTTSARGRVTCHTSAPLEFSRFVAYS	199
Qy	202	SAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSRL--RSLRTIAVVLTVFAVCFV	259
Db	200	SVMGLLFAVPPAVILVCYVLMARRLLKPAVGTSGGLPRAKRKSVRTIAVVLAVFALCFL	259
Qy	260	PFHITRTIYYLARLLEADCRVLNIUNVVYKVTPLASANSCLDPVLYLLTGDKYRRLRQ	319
Db	260	PFHVTRTLTYISFRSLDLSCHTLNAINMAYKVTPLASANSCLDPVLYFLAGORLVRFARD	319
Qy	320	LCGGGKQPRTAA	332
Db	320	AKPPTGSPATPA	332

Search completed: April 4, 2006, 20:14:09
Job time : 235 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2006, 20:14:22 ; Search time 47 Seconds
(without alignments)
642.056 Million cell updates/sec

Title: US-10-811-198-2

Perfect score: 1944

Sequence: 1 MASTESSLLRSLGLSPGPGS.....CRWAATPDQSCSTPRADRL 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/FCUTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-Result No.	Score	Query Match	Length	DB ID	Description
1	1944	100.0	365	2	US-09-745-842-16
2	1944	100.0	365	2	US-09-077-173D-2
3	1127.5	58.0	374	2	US-09-745-842-15
4	965	49.6	377	2	US-09-745-842-17
5	960.5	49.4	373	2	US-08-513-974B-373
6	955	48.1	374	2	US-09-102-710B-3
7	934	48.0	375	1	US-08-442-134A-2
8	934	48.0	375	1	US-08-444-581B-2
9	934	48.0	375	1	US-08-446-088A-2
10	934	48.0	375	1	US-08-559-524A-3
11	934	48.0	375	2	US-08-749-707-3
12	934	48.0	375	2	US-09-947-922-3
13	641.5	33.0	373	2	US-09-745-842-14
14	621	31.9	373	1	US-08-559-524A-4
15	621	31.9	373	2	US-08-749-707-4
16	621	31.9	373	2	US-09-947-922-4
17	619	31.8	362	2	US-08-513-974B-374
18	586	30.1	328	2	US-09-745-842-18
19	584.5	30.1	327	2	US-08-513-974B-372
20	584	30.0	328	2	US-08-513-974B-39
21	584	30.0	328	2	US-08-513-974B-371
22	584	30.0	328	2	US-09-461-436B-39
23	576	29.6	328	2	US-08-513-974B-56
24	576	29.6	328	2	US-08-513-974B-380
25	576	29.6	328	2	US-09-461-436B-56
26	571	29.4	328	2	US-08-459-046-2
27	571	29.4	328	2	US-09-102-710B-2

28	514	26.4	337	2	US-10-314-048A-28	Sequence 28, Appl
29	510	26.2	339	1	US-08-153-848-44	Sequence 44, Appl
30	510	26.2	339	1	US-08-812-871-3	Sequence 3, Appl
31	510	26.2	339	2	US-09-299-843A-44	Sequence 44, Appl
32	510	26.2	339	2	US-09-088-337B-44	Sequence 44, Appl
33	510	26.2	339	2	US-09-170-496D-32	Sequence 32, Appl
34	510	26.2	339	4	PCT-US93-11153-44	Sequence 44, Appl
35	510	26.2	339	4	PCT-US95-07180-2	Sequence 2, Appl
36	507	26.1	339	2	US-09-170-496D-182	Sequence 182, App
37	496.5	25.5	302	1	US-08-467-947A-30	Sequence 30, Appl
38	496.5	25.5	302	1	US-08-467-947A-30	Sequence 30, Appl
39	478.5	24.6	344	1	US-08-467-948A-8	Sequence 8, Appl
40	478.5	24.6	344	1	US-08-467-947A-8	Sequence 8, Appl
41	449.5	23.1	370	2	US-08-781-250-2	Sequence 2, Appl
42	424	21.8	395	1	US-08-097-938-2	Sequence 2, Appl
43	424	21.8	395	1	US-08-476-000-2	Sequence 2, Appl
44	424	21.8	395	1	US-08-472-840-2	Sequence 2, Appl
45	424	21.8	395	1	US-08-476-976-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-745-842-16
; Sequence 16, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Holloper, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y4 pyrimidinergic receptor
US-09-745-842-16

Query Match 100.0%; Score 1944; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASTESSLLRSLGLSPGSGSEVELDCWFDKFIPLVSYAVVFLGLGNAPTLLWF	60
Db	1	MASTESSLLRSLGLSPGSGSEVELDCWFDKFIPLVSYAVVFLGLGNAPTLLWF	60
Qy	61	IFRLRPWDATATYMFHLASDLYLVLSLPTLIYYAAHNPFGTEICKFVRFLFYNNLY	120
Db	61	IFRLRPWDATATYMFHLASDLYLVLSLPTLIYYAAHNPFGTEICKFVRFLFYNNLY	120
Qy	121	CSVLFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLAVLWAGCLVPNLFFVTTSSNGK	180
Db	121	CSVLFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLAVLWAGCLVPNLFFVTTSSNGK	180
Qy	181	TTVLCHDTPPEFDHYHVFSSAVMGLLFGVPCLTIVCYGLMARRLYQPLPGSAQSSSR	240
Db	181	TTVLCHDTPPEFDHYHVFSSAVMGLLFGVPCLTIVCYGLMARRLYQPLPGSAQSSSR	240
Qy	241	LRSLRTIAVLTVFAVCFVPHFTHRTIYYLARLEADCRVLNIYVNVVYKVRPLASANSC	300
Db	241	LRSLRTIAVLTVFAVCFVPHFTHRTIYYLARLEADCRVLNIYVNVVYKVRPLASANSC	300

; Sequence 15, Application US/09745842
; Patent No. 6762029

COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-581B-2

Query Match 48.0%; Score 934; DB 1; Length 375;
Best Local Similarity 58.5%; Pred. No. 6.4e-62;
Matches 183; Conservative 41; Mismatches 85; Indels 4; Gaps 3;
QY 22 EVELDCWDEDFKILLPVSYAVFVLGLGNAPTLMFLFRLRPWDATATYMFHLALSD 81
DB 20 ELGYRCRFNEDFKYLLPVSYGVVGVLCINAVGLYFLCLRLKTNASTTYMFLAVSD 79
QY 82 TLVLSLPLTYLYAAHNPFGTEICKFVRLFYNNLYCSVLFLTCISVHRYLCHPL 141
DB 80 ALYASLPLLVYYARGDHWPFSTVLCKLVRFLFYNNLYCSVLFLTCISVHRCLGLVRL 139
QY 142 RALRWGRPRLAGLLCLAVLWVAGCLVPLNLFVFTTSNKGTTVLCHDTPPEFDHYVFS 201
DB 140 RSLRWGRARYARRVAGVAVVVLACQAPVLYFTTSARG-PLTCHDTSAPELFSRFVAYS 198
QY 202 SAVMGLLFGVCLVTLVYCYLMARLYQPLPGSAQSSRL--RSLRTIAVLTAVFVAVCFV 259
DB 199 SVMGLLFAVPAVILVYCYLMARLLKPAYGTSGGLPRAKRSVRTIAVLAVALFALCF 258
QY 260 PPHITRTIYLLARLEADCRVLNVVYKVRPLASANSCLDPVLYLLTGDKYRRLRQ 319
DB 259 PFHVTRTLTYFSRSLDLSCHTLNAINMAYKVTR--LASANSCLDPVLYFLAGQLVRFARD 317
QY 320 LCGGKGPQRTAA 332
DB 318 AKPPTGSPATPA 330

RESULT 9
US-08-446-088A-2
Sequence 2, Application US/08446088A
Patent No. 5691156
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691156th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-088A-2

Query Match 48.0%; Score 934; DB 1; Length 375;
Best Local Similarity 58.5%; Pred. No. 6.4e-62;
Matches 183; Conservative 41; Mismatches 85; Indels 4; Gaps 3;
QY 22 EVELDCWDEDFKILLPVSYAVFVLGLGNAPTLMFLFRLRPWDATATYMFHLALSD 81
DB 20 ELGYRCRFNEDFKYLLPVSYGVVGVLCINAVGLYFLCLRLKTNASTTYMFLAVSD 79
QY 82 TLVLSLPLTYLYAAHNPFGTEICKFVRLFYNNLYCSVLFLTCISVHRYLCHPL 141
DB 80 ALYASLPLLVYYARGDHWPFSTVLCKLVRFLFYNNLYCSVLFLTCISVHRCLGLVRL 139
QY 142 RALRWGRPRLAGLLCLAVLWVAGCLVPLNLFVFTTSNKGTTVLCHDTPPEFDHYVFS 201
DB 140 RSLRWGRARYARRVAGVAVVVLACQAPVLYFTTSARG-PLTCHDTSAPELFSRFVAYS 198
QY 202 SAVMGLLFGVCLVTLVYCYLMARLYQPLPGSAQSSRL--RSLRTIAVLTAVFVAVCFV 259
DB 199 SVMGLLFAVPAVILVYCYLMARLLKPAYGTSGGLPRAKRSVRTIAVLAVALFALCF 258
QY 260 PPHITRTIYLLARLEADCRVLNVVYKVRPLASANSCLDPVLYLLTGDKYRRLRQ 319
DB 259 PFHVTRTLTYFSRSLDLSCHTLNAINMAYKVTR--LASANSCLDPVLYFLAGQLVRFARD 317
QY 320 LCGGKGPQRTAA 332
DB 318 AKPPTGSPATPA 330

RESULT 10
US-08-559-524A-3
Sequence 3, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-707-3

Query Match 48.0%; Score 934; DB 2; Length 375;
Best Local Similarity 58.5%; Pred. No. 6.4e-62;
Matches 183; Conservative 41; Mismatches 85; Indels 4; Gaps 3;

QY 22 EVELDCWDEDFKILLPVSYAVVVLGLGNAPTLMLFIPLRPMDATATYMFHLALSD 81
DB 20 ELGYRCRFNEDFKYLLPVSYGVVGVLCGLNAVGLYIFLCRLKTNASTTYMFHLAVSD 79
QY 82 TLVLSLPTLIYYAAAHNHWPFGTEICKVRFVFLFYNNLYCSVFLTICISVHRYLGICHPL 141
DB 80 ALYAASLPLLVYYVARGDHPFSTVLCKVRFVFLFYNNLYCSVFLTICISVHRCGLVLRPL 139
QY 142 RALRWGRPRLAGLLCLAVLWLVAGCLVPLNLFVTTSNKGTTLVLCDDTRPREPDHYVHS 201
DB 140 RSLRWGRARYARRVAGAVVWLVLACQAPVLYFVTTISARG-PLTCHDTSAPLFSRFVAYS 198
QY 202 SAVMGLLFGVCLTVLCYGLMARRLYQPLPGSAQSSRL--RSLRTIAVVLTVFAVCFV 259
DB 199 SVMGLLFAVFPFVILVCYVLMARLLKPAYGTSGGLPRAKRSVRTIAVVLAVFALCFL 258
QY 260 PFHITRTIYLARLLEADCRVLNIVNVVYKVRPLASANSCLDPVLYLLTGDKYRRQLRQ 319
DB 259 PFHVTRTLIFSRLSLSCHTLNAINMAYKVTR-LASANSCLDPVLYFLAGQLRVRFARD 317
QY 320 LCGGKQPQRTAA 332
DB 318 AKPPTGSPATPA 330

RESULT 12
US-09-947-922-3
Sequence 3, Application US/09947922
Patent No. 6680373
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-3

Query Match 48.0%; Score 934; DB 1; Length 375;
Best Local Similarity 58.5%; Pred. No. 6.4e-62;
Matches 183; Conservative 41; Mismatches 85; Indels 4; Gaps 3;

QY 22 EVELDCWDEDFKILLPVSYAVVVLGLGNAPTLMLFIPLRPMDATATYMFHLALSD 81
DB 20 ELGYRCRFNEDFKYLLPVSYGVVGVLCGLNAVGLYIFLCRLKTNASTTYMFHLAVSD 79
QY 82 TLVLSLPTLIYYAAAHNHWPFGTEICKVRFVFLFYNNLYCSVFLTICISVHRYLGICHPL 141
DB 80 ALYAASLPLLVYYVARGDHPFSTVLCKVRFVFLFYNNLYCSVFLTICISVHRCGLVLRPL 139
QY 142 RALRWGRPRLAGLLCLAVLWLVAGCLVPLNLFVTTSNKGTTLVLCDDTRPREPDHYVHS 201
DB 140 RSLRWGRARYARRVAGAVVWLVLACQAPVLYFVTTISARG-PLTCHDTSAPLFSRFVAYS 198
QY 202 SAVMGLLFGVCLTVLCYGLMARRLYQPLPGSAQSSRL--RSLRTIAVVLTVFAVCFV 259
DB 199 SVMGLLFAVFPFVILVCYVLMARLLKPAYGTSGGLPRAKRSVRTIAVVLAVFALCFL 258
QY 260 PFHITRTIYLARLLEADCRVLNIVNVVYKVRPLASANSCLDPVLYLLTGDKYRRQLRQ 319
DB 259 PFHVTRTLIFSRLSLSCHTLNAINMAYKVTR-LASANSCLDPVLYFLAGQLRVRFARD 317
QY 320 LCGGKQPQRTAA 332
DB 318 AKPPTGSPATPA 330

RESULT 11
US-08-749-707-3
Sequence 3, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

```

:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/947,922
: FILING DATE: 07-Sep-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/749,707
: FILING DATE: 15-NOV-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Adler, Reid G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 044481-5010-01-US
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-467-7000
: TELEFAX: 202-467-7176
:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 375 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
: US-09-947-922-3

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Query Match	48.0%;	Score 934;	DB 2;	Length 375;
Best Local Similarity	58.5%;	Pred. No. 6.4e-62;		
Matches 183;	Conservative 41;	Mismatches 85;	Indels 4;	Gaps 3

Qy	22	EVELDCWFDEQFKILLPVSVAVFVLGVLGNAPTLWLFIPLRPWDATATYMEHLALSD	81
Db	20	ELGTRCRNEDFKYILLPVSYGVCVLGCLNAVLGIIFCLRLKTNASTTTNMFHLAVSD	79
Qy	82	TLYVLSLPTLIYYAAHNHPFGTEICKFVRFLFYWNLYCSVLFLTCTISVHRVYLGIICHL	141
Db	80	ALYAASLPLLYYYARGDHPPESTVCKLVRELFYTNLYCSILFLTCTISVHRCLGVRLP	139
Qy	142	RALKWGRPLAGLLCLAVLWVAGCIVLNPFLFVTTSTNKGTTVLCDDTTPPEBFDHYVHS	201
Db	140	RSLRWGRARYARRVAGAVWVLVLAQAPVLYFVTTTSARG-PLTCHDTSAPELFSRFVAYS	198
Qy	202	SAVMCLLFGVCEVTLVCYGLMARLYOPLPSGAQSSRL--RSLRTIAVILTVFAVCFV	259
Db	199	SVMLGLLFAVPFAVTLVCVILMARLLPAYGTSGGLPRAKRSVRTIAVILAVFALCPFL	258
Qy	260	PFHITRTYYLARLLEADCVRVLNIWVWYKVRPLASANSCLDDPVLYLLTGDKYERQLRQ	319
Db	259	PFHVRTLYYFSRDLDSCHTLNAINMAYKVR-LASANSCLDDPVLYFLAGORLYRFARD	317
Qy	320	LCGGGKQPQRTAA	332
Db	318	AKPPTGSPATPA	330

LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

Query Match 31.9%; Score 621; DB 1; Length 373;
Best Local Similarity 43.4%; Pred. No. 1.le-38;
Matches 126; Conservative 53; Mismatches 103; Indels 8; Gaps 4;

QY 33 EKFIILPVSYAVFVLGLGNAPTLWLFIFRLRPWDATATYMFHLALSDTLVLSLPTLI 92
DB 49 FQFYILPAVYILVFIIGLGNVAIMFVFMKPSGISVYMFNLALADFLVLTLPALI 108
QY 93 YYYAAHNPFGTEICKFVRFVFNLYCSVLFTICISVHRYLGICHPRLALRWGRPRLA 152
DB 109 FYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFTICISAHRYSGVVYPLKSLGRKKQNA 168
QY 153 GLLCLAVMLVWAGCLVPLNLPFVTTTS-NKGTTVLCHDTRPEEFHDVHVFSSAVMGLLFGV 211
DB 169 VVISVLVWLVVVGISPLFYSYGTGIRKNKTIITCYDTSDEYLSRYSFIYSMCTTVAMFCV 228
QY 212 PCLVTLVCYGLMARRL-YQPLPGSAQSSRLSLRTIAVLTAVFVCFVFPFHITRIYYL 270
DB 229 PLVLILGCYGLIVRALIYKOLD--NSPLRKSIVLIVLTVFAVSYIPFHVMTNLR 285
QY 271 ARL---LEADCRVLNIVNVVYKVRPLASANSCLDPVLYLLTGDKYRROL 317
DB 286 ARLDQTPMCAFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRL 335

RESULT 15
US-08-749-707-4
Sequence 4, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-707-4

Query Match. 31.9%; Score 621; DB 2; Length 373;
Best Local Similarity 43.4%; Pred. No. 1.le-38;
Matches 126; Conservative 53; Mismatches 103; Indels 8; Gaps 4;
QY 33 EKFIILPVSYAVFVLGLGNAPTLWLFIFRLRPWDATATYMFHLALSDTLVLSLPTLI 92
DB 49 FQFYILPAVYILVFIIGLGNVAIMFVFMKPSGISVYMFNLALADFLVLTLPALI 108
QY 93 YYYAAHNPFGTEICKFVRFVFNLYCSVLFTICISVHRYLGICHPRLALRWGRPRLA 152
DB 109 FYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFTICISAHRYSGVVYPLKSLGRKKQNA 168
QY 153 GLLCLAVMLVWAGCLVPLNLPFVTTTS-NKGTTVLCHDTRPEEFHDVHVFSSAVMGLLFGV 211
DB 169 VVISVLVWLVVVGISPLFYSYGTGIRKNKTIITCYDTSDEYLSRYSFIYSMCTTVAMFCV 228
QY 212 PCLVTLVCYGLMARRL-YQPLPGSAQSSRLSLRTIAVLTAVFVCFVFPFHITRIYYL 270
DB 229 PLVLILGCYGLIVRALIYKOLD--NSPLRKSIVLIVLTVFAVSYIPFHVMTNLR 285
QY 271 ARL---LEADCRVLNIVNVVYKVRPLASANSCLDPVLYLLTGDKYRROL 317
DB 286 ARLDQTPMCAFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRL 335

Search completed: April 4, 2006, 20:15:48
Job time : 48 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 20:10:27 ; Search time 41 Seconds
(without alignments)
856.564 Million cell updates/sec

Title: US-10-811-198-2
Perfect score: 1944
Sequence: 1 MASTSSLRLSLGLSPGPGS.....CRWAATPDSSCSCTPRADRL 365

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1944	100.0	365	2 S68679	G protein-coupled
2	962.5	49.5	373	2 A47556	ATP receptor P2u -
3	934	48.0	375	2 A54946	P-2U nucleotide re
4	641.5	33.0	373	2 JC4737	G protein-coupled
5	628	32.3	362	2 S33733	G protein-coupled
6	621	31.9	373	2 JCA162	P2Y receptor - bov
7	588	30.2	328	2 I55450	G protein-coupled
8	586	30.1	328	2 JC4800	P2Y6 receptor - hu
9	501.5	25.8	308	2 I50241	G protein-coupled
10	479.5	24.7	344	2 T09508	intron 17 purinerg
11	450.5	23.2	370	2 JC5549	heptahelical P2Y5-
12	423	21.8	399	2 I48705	proteinase activat
13	411.5	21.2	420	2 I51667	thrombin receptor
14	403	20.7	397	2 S65518	proteinase-activat
15	400	20.6	372	2 I38532	delta opioid recep
16	397.5	20.4	425	2 A37912	thrombin receptor
17	388.5	20.0	427	2 S17148	alpha-thrombin rec
18	388	20.0	432	2 A43448	thrombin receptor
19	385	19.8	372	2 S34592	delta opioid recep
20	383	19.7	361	2 B45680	G protein-coupled
21	382.5	19.7	362	2 JN0694	angiotensin II rec
22	381.5	19.6	398	2 I56504	mu opioid receptor
23	378.5	19.5	392	2 S65693	opioid receptor mu
24	378.5	19.5	400	2 I56553	mu opiate receptor
25	377	19.4	372	2 B48227	delta opioid recep
26	376.5	19.4	398	2 I56517	mu opioid receptor
27	371.5	19.1	342	2 A40191	platelet-activatin
28	371.5	19.1	398	2 A57510	mu opioid receptor
29	370.5	19.1	359	2 JCS277	G protein-coupled

30	369.5	19.0	359	2 JH0621	angiotensin II rec
31	366	18.8	363	2 I57955	somatostatin recep
32	366	18.8	364	2 J0763	somatostatin recep
33	364.5	18.8	359	2 JC2134	angiotensin II rec
34	363	18.7	359	2 A42656	angiotensin II rec
35	362	18.6	362	2 S68207	G protein-coupled
36	361	18.6	354	2 I53033	G protein-coupled
37	360.5	18.5	359	2 S44425	angiotensin II rec
38	360	18.5	359	2 JC1104	angiotensin II rec
39	359	18.5	362	2 A57641	G protein-coupled
40	358.5	18.4	359	2 S15403	angiotensin II rec
41	357	18.4	380	2 S36143	kappa opioid recep
42	356	18.3	359	2 A48857	angiotensin II rec
43	356	18.3	380	2 JC2338	kappa opioid recep
44	355	18.3	359	2 I39418	angiotensin II rec
45	355	18.3	380	2 A55259	kappa opioid recep

ALIGNMENTS

RESULT 1

S68679

G protein-coupled receptor - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S68679

R:Stam, N.J.; Kloppe, J.; van de Heuvel, M.; Olijve, W.

FBBS Lett. 384, 260-264, 1996

A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) exp:

A:Reference number: S68679; MUID:96197801; PMID:8617367

A:Accession: S68679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STA>

A:Cross-references: UNIPROT:P51582; UNIPARC:UPI00002E776; EMBL:X96597; NID:G1296631; 1

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor

Query Match 100.0%; Score 1944; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 9.8e-165;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASTSSLRLSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFLGLGNAPTLWLF	60
DB	1	MASTSSLRLSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFLGLGNAPTLWLF	60
QY	61	IFRLRPWDATATYMPHLALSDTLVLSLPTLIYYAAHNNHWPFGTEICKFVFLFYNNLY	120
DB	61	IFRLRPWDATATYMPHLALSDTLVLSLPTLIYYAAHNNHWPFGTEICKFVFLFYNNLY	120
QY	121	CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLCLAVLVVAGCLVNLFPVFTTSNKG	180
DB	121	CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLCLAVLVVAGCLVNLFPVFTTSNKG	180
QY	181	TTVLCHDTRPEEFHYHFSSAVNGLLFGVPCPLTVLCYGLMARLYOPLPGSAOSSR	240
DB	181	TTVLCHDTRPEEFHYHFSSAVNGLLFGVPCPLTVLCYGLMARLYOPLPGSAOSSR	240
QY	241	LRSLRTIAVLTVAFCVFPFHITRTIYYLARLLADCRVLMNVVYVYKTRPLASANS	300
DB	241	LRSLRTIAVLTVAFCVFPFHITRTIYYLARLLADCRVLMNVVYVYKTRPLASANS	300
QY	301	LDPVLYLLTGKYYRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSPT	360
DB	301	LDPVLYLLTGKYYRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSPT	360
QY	361	RADRL 365	
DB	361	RADRL 365	

RESULT 2

A47556
ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47556
R;Lustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFF; GB:L14751; NID:g309457; PIDN:
A;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

Query Match 49.5%; Score 962.5; DB 2; Length 373;
Best Local Similarity 53.7%; Pred. No. 1.1e-77;
Matches 188; Conservative 46; Mismatches 97; Indels 19; Gaps 3;

QY 22 EVELDCWFDEDFKIFLLPVSYAVVFLGLGNAPTLWLFIFLRPMDATATYMFHLALSD 81
DB 20 ELGYKCFNEDEKIVLLPVSYGVVGVGLCLNVAAGLYIFLCRLKTNASTTYMFHLAVSD 79
QY 82 TLVLSLPTLIYYAAHNHPFGTEICKFVRFLEFYNLYCSVLFLTCISVHRVILGICHPL 141
DB 80 SLVLAASLPLLVVYARGDHPFSTVLCKLVRFLEFYNLYCSVLFLTCISVHRVILGICHPL 139
QY 142 RALRWGRPRLAGLLCLAVLWLVVAGLVNLPVFFVTTNKGTTVLCHDTRPEEDHVVHFS 201
DB 140 HSLRWGRARVARRVAVVWLVLAQAPVLYFVTTISVGRITRCHDTSARELSFHFVAYS 199
QY 202 SAVMGLLFGVPCLVTLVVCYGLMARLYQPLPGSAQSSRL--RSLRTIAVLVTVFAVCFV 259
DB 200 SVMGLLFAVPFVILVVCVLMARLLKPAVGTGGPRAKRKSVRTIALVLAVALCFPL 259
QY 260 PFHITRTIYLARLLEADCRVLNVVNVVYKVRPLASANSCLDPVLYLLTGDKYRQLRQ 319
DB 260 PFHITRTIYLSFRSLDLSCHTLNAINMAYKVTIR--LASANSCLDPVLYFLAGQLRVRFARD 319
QY 320 LCGGKGPQPRTAA 332
DB 320 AKPPTGSPATPA 330

RESULT 3
A54946
P-2U nucleotide receptor - human
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C;Accession: A54946
R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A;Reference number: A54946; MUID:94211846; PMID:8159738
A;Accession: A54946
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-375 <PAR>
A;Cross-references: UNIPARC:UPI0000145104; GB:U07225
A;Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
A;Gene: GDB:P2RY2; HP2U; P2U
A;Cross-references: GDB:362713; OMIM:600041
A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.0%; Score 934; DB 2; Length 375;
Best Local Similarity 58.5%; Pred. No. 3.6e-75;
Matches 183; Conservative 41; Mismatches 85; Indels 4; Gaps 3;

QY 22 EVELDCWFDEDFKIFLLPVSYAVVFLGLGNAPTLWLFIFLRPMDATATYMFHLALSD 81
DB 20 ELGYKCFNEDEKIVLLPVSYGVVGVGLCLNVAAGLYIFLCRLKTNASTTYMFHLAVSD 79
QY 82 TLVLSLPTLIYYAAHNHPFGTEICKFVRFLEFYNLYCSVLFLTCISVHRVILGICHPL 141
DB 80 ALVLAASLPLLVVYARGDHPFSTVLCKLVRFLEFYNLYCSVLFLTCISVHRVILGICHPL 139
QY 142 RALRWGRPRLAGLLCLAVLWLVVAGLVNLPVFFVTTNKGTTVLCHDTRPEEDHVVHFS 201
DB 140 RSLRWGRARVARRVAVVWLVLAQAPVLYFVTTISVARG--PLTCHDTSARELSFHFVAYS 198
QY 202 SAVMGLLFGVPCLVTLVVCYGLMARLYQPLPGSAQSSRL--RSLRTIAVLVTVFAVCFV 259
DB 199 SVMGLLFAVPFVILVVCVLMARLLKPAVGTGGPRAKRKSVRTIALVLAVALCFPL 258
QY 260 PFHITRTIYLARLLEADCRVLNVVNVVYKVRPLASANSCLDPVLYLLTGDKYRQLRQ 319
DB 259 PFHITRTIYLSFRSLDLSCHTLNAINMAYKVTIR--LASANSCLDPVLYFLAGQLRVRFARD 317
QY 320 LCGGKGPQPRTAA 332
DB 318 AKPPTGSPATPA 330

RESULT 4
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Commun, D.; Firoctton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900; UNIPARC:UPI0000001C06; GB:S81950; NID:g1839438; PI:
R;Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.
Biochem. Biophys. Res. Commun. 218, 783-786, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AY>
A;Cross-references: UNIPARC:UPI0000001C06; GB:U42029; NID:g1147730; PIDN:AAA97872.1; P:
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: UNIPARC:UPI000016A5B9; EMBL:Z49205; NID:g798835; PIDN:CAA89086.1;
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It respon
C;Genetics:
A;Gene: P2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;258/336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;330/339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen

Query Match 33.0%; Score 641.5; DB 2; Length 373;
Best Local Similarity 40.0%; Pred. No. 3.1e-49;
Matches 140; Conservative 60; Mismatches 121; Indels 29; Gaps 9;

QY 17 GPSS-----EVELDWFDE-DFKILLPVSYAVVFLGLNAPTLWLFI 63
DB 20 GPSSGNGNSTVASTAAVSSFKKATKTGFQFYLPAYILVFIIFGLNSVAIMMVF 79
QY 64 LRPWDATATYMHFALSDTLVLSPLTIYVYAAHNPFGTEICKVRFVWNLVCSV 123
DB 80 MKPWSGISVYMNALADFLVLTLPALIFYYFNKTDWIFGDAMCKLQRFHVNLYGSI 139
QY 124 LFTICISVHYLGICHLRALRWRGRPLAGLLCIA--VWLVAGCLVPNLFVFTTS--NKG 180
DB 140 LFTICISAHRYSGVYPLKSL--GRKKNAICISVLVWLVVAISPIIFYSGTVGRKN 197
QY 181 TTVLCHDTPPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARL-YQPLPGSAQSSS 239
DB 198 KTICTYDTSDEYLSRYFYISYCTTAMFCVPLVILGICYGLVRLIYKDLN---NSPL 254
QY 240 RLRSRTIAVLTVAFCVFPFHRTIYTLARL---LEADCRVLIINVVYKTRPLAS 296
DB 255 RRSKIYLIIVLTVAFSYIFPHVMTNLRARLDFOTPMCAFNDKRVATYQVTRGLAS 314
QY 297 ANSCLDPVLYLLTGDKYRQL-----RQLCGGKQPQPRTAASSLALVSLPE 342
DB 315 LNSCVDPIYFLAGDTFRRLSRATRKSRSEANLQSKSDTTLNLP 364

RESULT 5
S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A:Reference number: S33733; MUID:93285340; PMID:8508924
A:Accession: S33733
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <WEB>
A:Cross-references: UNIPROT:P34996; UNIPARC:UPI00000405D4; EMBL:X73268; NID:g395084; PID
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 32.3%; Score 628; DB 2; Length 362;
Best Local Similarity 39.4%; Pred. No. 4.8e-48;
Matches 137; Conservative 62; Mismatches 133; Indels 16; Gaps 7;

QY 4 TESSILRSGLSPGSSSEVELDCWDEDFKFIPLPVSYAVVFLGLNAPTLWLFI 63
DB 13 TQPELLAG--GWAAGNATTKCSLT---KTGFQFYLPAYILVFIIFGLNSVAIMMVF 68
QY 64 LRPWDATATYMHFALSDTLVLSPLTIYVYAAHNPFGTEICKVRFVWNLVCSV 123
DB 69 MKPWSGISVYMNALADFLVLTLPALIFYYFNKTDWIFGDVWCKLQRFHVNLYGSI 128
QY 124 LFTICISVHYLGICHLRALRWRGRPLAGLLCIAVWLVVAGCLVPNLFVFTTS--NKGTT 182
DB 129 LFTICISVHYTGTVGHVPLKSLGRKKNAVYVSSLVWLVVAIVIAPIIFYSGTVGRNKT 188
QY 183 VLCHDTPPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARL-YQPLPGSAQSSSL 241
DB 189 ITCYDTPADYLSRYFVYSMCTTVMFCIPFIVILGICYGLVRLIYKDLN---NSPLRR 245
QY 242 RLRSRTIAVLTVAFCVFPFHRTIYTLARL---LEADCRVLIINVVYKTRPLAS 298

DB 246 KSIYLVLIIVLTVAFSVLPVHVMKTLNLRARLDFOTPMCAFNDKRVATYQVTRGLASLN 305
QY 299 SCLDPVLYLTGDKYRQL-----RQLCGGKQPQPRTAASSLALVSLPE 342
DB 306 SCVDPIYFLAGDTFRRLSRATRKSRSENPVQSKSEMTNLTLE 353

RESULT 6
JC4162
P2Y receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: JC4162
R:Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A:Title: Cloning and characterisation of a bovine P2Y receptor.
A:Reference number: JC4162; MUID:95352058; PMID:7626079
A:Accession: JC4162
A:Molecule type: mRNA
A:Residues: 1-373 <HEN>
A:Cross-references: UNIPROT:P48042; UNIPARC:UPI000004BEDB; EMBL:X87628; NID:gl032484;
A:Experimental source: aortic endothelial cell
C:Genetics:
A:Gene: bovP2Y
C:Superfamily: ATP receptor P2u
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carboxylate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 31.9%; Score 621; DB 2; Length 373;
Best Local Similarity 43.4%; Pred. No. 2.1e-47;
Matches 126; Conservative 53; Mismatches 103; Indels 8; Gaps 4;

QY 33 FKFIPLPVSYAVVFLGLNAPTLWLFIIFLRPMDATATYMHFALSDTLVLSPLTLI 92
DB 49 FQFYLPAYILVFIIFGLNSVAIMMVFHMKPWSGISVYMNALADFLVLTLPALI 108
QY 93 YTYAHHNPFGTEICKVRFVWNLVCSVLFYCNLYSVLFLFCISVHYLGICHLRALRWRGRPLA 152
DB 109 FYFNKTDWIFGDAMCKLQRFIFHVNLYGSIILFLTCISAHRYSGVYVPLKSLGRKKQNA 168
QY 153 GLLCLAVMLVWAGCLVPNLFVFTTS--NKGTTVLCHDTPPEEDHYVHSSAVMGLLGV 211
DB 169 VYISVLWLIIVVVGISPIIFYSGTGIRKNKTICTYDTSDEYLSRYFYISYCTTVMFCV 228
QY 212 PCLVTLVYGLMARL-YQPLPGSAQSSSLRSLRTIAVLTVAFCVFPFHRTIYTL 270
DB 229 PLVLILGICYGLVRLIYKDLN---NSPLRRKSIYLIIVLTVAFSYIPFHVMTNLR 285
QY 271 ARL---LEADCRVLIINVVYKTRPLASANSCLDPVLYLLTGDKYRQL 317
DB 286 ARLDQTPMCAFNDKRVATYQVTRGLASLNSCVDPIYFLAGDTFRRL 335

RESULT 7
I55450
G protein-coupled P2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55450
R:Chang, K.; Hanaka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.
A:Reference number: I55450; MUID:96064682; PMID:7592819
A:Accession: I55450
A:Status: preliminary; translated from GB/EMBL/DBJ

DB 2 VSSNCSTEDSFRIITLIGCVFNVFVLTGHTANCVALLIITLTAIVAG.....TANSTSTST


```

:::
308 LLVHYFLIKTORQSHVY-----ALYVALCSTLNSCIDPFVYVYFVKDFRDHARNALLC 363
322 GGGKQPQRTAASSLALVSLPDSRCRWATPDSSCS 358
364 RSVTVNRMQ-----ISLSSNKFGRKSGSYSSSTS 394

RESULT 13
151667
thrombin receptor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51667
R:Gerzsten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A:Reference number: I51667; MUID:94195429; PMID:8145852
A:Accession: I51667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-420 <GER>
A:Cross-references: UNIPROT:P47749; UNIPARC:UPI0000131316; EMBL:U09632; NID:G495197; PID
Query Match 21.2%; Score 411.5; DB 2; Length 420;
Best Local Similarity 29.7%; Pred. No. 8.7e-29;
Matches 98; Conservative 61; Mismatches 144; Indels 27; Gaps 7;
QY 34 KFLLPVSVAVYVGLGNGAPTLMLFIFRLRPWDATATYMPHLALSDTLVLSLPTLIY 93
-D 102 KPV--PSLYTVVFIYGLPFLNLLAIIFLEKVKRPAPVYMLNLAIAADVFFVSLPFKIA 159
QY 94 YYAANHNPFGTEICKFVRFLFYMLYCSVLFTLCISVHRVYLGICHPRLALRWGRPRLAG 153
D 160 YHLSGNDMLFGPGMKRIVTAIFYCNMYCSVLIIASISVDRFLAVVYPMHLSLSWRTMSRAY 219
QY 154 LCLAVWLAVAGCLVPLNLPFVTTSN--KGTIVLCHDTTRPEEF-DHYVHFSSAVNGLFG 210
D 220 MACSPFWLISASTIPLLVTEQTKIPRLDITTCVDLDLKDOLFVFIYFSSFCLLPFF 279
QY 211 VPLCLVLCVGLMARRLVQPLPGSAQSSRLSLRTIAVLTFAVFCVPFPHITRTIYL 270
D 280 VFFITITCYIGIIRSLSS--SSIENCKKRALFLAVVLCVFIICPGPITNVLFLTHYL 337
QY 271 AFLLEADCRVLNVVYVYKVRPLASANSCLDPVLYLTGDKYRQLRQ-LCGGKGKQOPR 329
D 338 QEANE-----FLYFAYILSACVGSVSCCLDPLIYVYASSQCORYLYSLLCCKRVSPFG 390
QY 330 TAASSIALVSLPDSRCRWATPDSSCSST 359
D 391 SSTGLMSTAMKND-----NCST 408

RESULT 14
S66518
proteinase-activated receptor 2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66518; S64709; G02131
R:Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A:Title: Molecular cloning and functional expression of the gene encoding the human prot
A:Reference number: S66518; MUID:96048032; PMID:7556175
A:Accession: S66518
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <N>S>
A:Cross-references: UNIPROT:P55085; UNIPARC:UPI0000131317; EMBL:Z49993; NID:G1008084; PI
R:Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn
Biochem. J. 314, 1009-1016, 1996
A:Title: Molecular cloning, expression and potential functions of the human proteinase-a
A:Reference number: S64709; MUID:96177879; PMID:8615752
A:Accession: S64709
```

```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137; 'A', 139-397 <BO>S>
A:Cross-references: UNIPARC:UPI0000050430; EMBL:U34038; NID:G1041728; PIDN:AA847871.1;
A:Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue
R:Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A:Reference number: H00822
A:Accession: G02131
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 29-397 <KAH>
A:Cross-references: UNIPARC:UPI000016A259; EMBL:U36753; NID:G1208539; PIDN:AAA90957.1;
C:Genetics:
A:Map position: 5q13
A:Introns: 28/1
C:Superfamily: ATP receptor P2u
F:1-36/Domain: activation peptide #status predicted <A>P>
F:1-25/Domain: signal sequence #status predicted <SIG>
F:37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>
Query Match 20.7%; Score 403; DB 2; Length 397;
Best Local Similarity 32.1%; Pred. No. 4.7e-28;
Matches 95; Conservative 57; Mismatches 124; Indels 20; Gaps 9;
QY 36 ILPLPVSVAVYVGLGNGAPTLMLFIFRLRPWDATATYMPHLALSDTLVLSLPTLIY 95
D 76 VFLPVIYTVVFGVGLGNGAPTLMLFIFRLRPWDATATYMPHLALSDTLVLSLPTLIY 135
QY 96 AAHNHPFGTEICKFVRFLFYMLYCSVLFTLCISVHRVYLGICHPRLALRWGRPRLAG 155
D 136 IHGNWLYGEALCNVLIIGFFYGNMYCSILFTWCLSVQRYVYVNPVPMGHSR-KKANIALGI 194
QY 156 CLAVWLAVAGCLVPLNLPFVTTSN--KGTIVLCHDTTRPEEF-DHYVHFSSAVNGL 207
D 195 SLAIWLLILLVTPILYVYVKTIFIPALNITT--CHDVL-PEQLLVGDMFYFLSLAIG- 249
QY 208 LFGVPCVLCVGLMARRLVQPLPGSAQSSRLSLRTIAVLTFAVFCVPFPHITRTI 267
D 250 VFLPFAELTASVYVIMIRMLRSSANDENSEKKRRAIKLIVTVLWYLCITFPNSLLV 309
QY 268 YLARLEADCRVLNVVYVYKVRPLASANSCLDPVLYLTGDKYRQLRQ--LC 321
D 310 HYP--LKSQO--SHYVALYIVALCLSTLNSCIDPFVYVYFVKDFRDHARNALLC 361

RESULT 15
I38532
delta opioid receptor - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38532; I38657
R:Knapp, R.J.; Malatynska, E.; Pang, L.; Xiaoping, L.; Nguyen, M.; Santoro, G.; Varga,
Life Sci. 54, PL463-PL469, 1994
A:Title: Identification of a human delta opioid receptor: Cloning and expression.
A:Reference number: I38532; MUID:94260835; PMID:8201839
A:Accession: I38532
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <KNA>
A:Cross-references: UNIPROT:P41143; UNIPARC:UPI00000503F7; EMBL:U07882; NID:G497313; P
R:Simonin, F.; Befort, K.; Gavériaux-Ruff, C.; Matthes, H.; Nappay, V.; Lannes, B.; Mi
Mol. Pharmacol. 46, 1015-1021, 1994
A:Title: The human delta-opioid receptor: genomic organization, cDNA cloning, function
A:Reference number: I38657; MUID:95107267; PMID:7808419
A:Accession: I38657
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-26; 'C', 28-39, 'AR', 42-347, 'A', 349-369, 'A', 371-372 <SIM>
A:Cross-references: UNIPARC:UPI0000130D94; EMBL:U10504; NID:G501144; PIDN:AAA83426.1;
C:Genetics:
A:Gene: GDB:OPRD1
A:Cross-references: GDB:I37215; OMIM:165195
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A:Map position: lp36.1-1p34.3

C:Superfamily: vertebrate rhodopsin

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Query Match      20.6%; Score 400; DB 2; Length 372;
Best Local Similarity 31.2%; Pred. No. 8.1e-28;
Matches 112; Conservative 57; Mismatches 138; Indels 52; Gaps 11;

Qy 16 PGPGS-SEVELDCWFDEDFKELLPSVAVFVLGVLGNAPTLLFLFRLREWDATATYM 74
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 38 PGPGSASSLAL-----AIAIYALYSAVCAVGLGNLGVFGIVRYTKMTATNIYI 88
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 75 FHLALSDTLIYVLSPTLIYYAAHNPFGTEICKFVRFLFYNNLYCSVLFITCISVHRY 134
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 89 FNLALADALATSTLFFQSAYLMEF-WPFGELLCKAVLSIDYNNMFTSIFTLTWMSVDY 147
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 135 LGICHPLRALRWGRPRLAGLLCLAVLVVAGCLVPLNFVTTSNKGTTLVCHDTRPEEF 194
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 148 IAVCHPVKALDPRTPAKAKLINICITWLASGVGPIMVMAVTRPRDGAVVC----- 198
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 DHYVHFSS-----AVMGLLFGVPCLVTLVCYGLMARLL--YQPLPGSAQSSRL 241
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 199 --MLQFPSPSWYWDVTWKICVFLFAFVVPILITTCYGLMLLRSLRSVRLLSGSKEDRSL 256
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 242 RSL-RTIAVLTAVFVCFVPHITRTIYVLARLLEADCRVLNIVNVYKVTPLASANSC 300
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 257 RRIETMVLVVGAFFVVCWAPIHIFVIVTLVDIDREDPLVVAALHLCI-----ALGYANSS 312
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 301 LDPVLYLTGDKYRQLQLCGG--GKPOPTAASSLALVSLPEDSSCR---WAATPOD 354
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 313 LNPVLYAFLDENFKRCFQLCKPCGRPDPS-----FSRPREATARERTACTPSD 364
Db : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: April 4, 2006, 20:14:54

Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 20:26:42 ; Search time 25 Seconds
(without alignments)
444.452 Million cell updates/sec

Title: US-10-811-198-2

Perfect score: 1944

Sequence: 1 MASTESSLLRSLGSLPGSGS.....CRWAATPDSCSTPADRL 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 8: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	100.0	365	6	US-10-995-561-545
2	641.5	33.0	373	7	US-11-127-877-46
3	641.5	33.0	373	7	US-11-222-874-6
4	515	26.5	367	7	US-11-157-930-6
5	514	26.4	337	7	US-11-222-874-2
6	510	26.2	339	7	US-11-157-930-4
7	403	20.7	397	7	US-11-072-175-145
8	397.5	20.4	485	6	US-10-821-234-934
9	388.5	20.0	370	6	US-10-330-773-446
10	378.5	19.5	400	7	US-11-127-877-55
11	377.5	19.4	346	7	US-11-157-930-2
12	375	19.3	368	6	US-10-920-055-6
13	375	19.3	415	7	US-11-017-058-2
14	367	18.9	357	7	US-11-261-135-2
15	362.5	18.6	380	6	US-10-330-773-443
16	361	18.6	359	6	US-10-876-787-2
17	360	18.5	359	6	US-10-995-561-712
18	360	18.5	359	6	US-10-995-561-716
19	360	18.5	359	7	US-11-127-877-65
20	360	18.5	388	6	US-10-995-561-713
21	360	18.5	394	6	US-10-995-561-714
22	360	18.5	394	6	US-10-995-561-715
23	345.5	17.8	254	6	US-10-055-877-248
24	345.5	17.8	254	6	US-10-055-877-327
25	345.5	17.8	254	6	US-10-055-877-340

26	345.5	17.8	254	6	US-10-877-346-83	Sequence 83, Appl
27	345.5	17.8	337	7	US-11-157-930-5	Sequence 5, Appl
28	343	17.6	388	6	US-10-995-561-838	Sequence 838, App
29	343	17.6	389	6	US-10-995-561-837	Sequence 837, App
30	342	17.6	371	6	US-10-501-035-242	Sequence 242, App
31	341	17.5	353	7	US-11-017-058-9	Sequence 9, Appl
32	333.5	17.2	350	7	US-11-249-847-546	Sequence 546, App
33	332.5	17.1	380	7	US-11-210-139-17	Sequence 17, Appl
34	330	17.0	375	7	US-11-127-877-67	Sequence 67, Appl
35	327.5	16.8	352	7	US-11-028-922A-1	Sequence 1, Appl
36	327.5	16.8	355	7	US-11-218-281-26	Sequence 26, Appl
37	325	16.7	337	7	US-11-166-412-60	Sequence 60, Appl
38	322	16.6	355	7	US-11-068-686-4	Sequence 4, Appl
39	322	16.6	355	7	US-11-127-877-64	Sequence 64, Appl
40	322	16.6	355	7	US-11-216-610-2	Sequence 2, Appl
41	322	16.6	355	7	US-11-216-610-4	Sequence 4, Appl
42	321.5	16.5	349	7	US-11-028-922A-2	Sequence 2, Appl
43	321	16.5	259	6	US-10-055-877-225	Sequence 225, App
44	321	16.5	259	6	US-10-055-877-237	Sequence 237, App
45	321	16.5	259	7	US-11-206-587-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-995-561-545

; Sequence 545, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 545

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-995-561-545

Query Match

Best Local Similarity 100.0%; Score 1944; DB 6; Length 365;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASTESSLLRSLGSLPGSGSEVELDCWDFDKFILLPVSYAVVVLGLGNAPTLLWF	60
Db	1	MASTESSLLRSLGSLPGSGSEVELDCWDFDKFILLPVSYAVVVLGLGNAPTLLWF	60
Qy	61	IFRLRPWDATATYMFHLASDITLVLSLPTLIYYAAHNNHWPFGTEICKFVRFLFYNNLY	120
Db	61	IFRLRPWDATATYMFHLASDITLVLSLPTLIYYAAHNNHWPFGTEICKFVRFLFYNNLY	120
Qy	121	CSVLFLTCISVHRVYLGICHPRLALRWGRPRLAGLLCLAVMLVWAGCLVPLNLFVYTSNKG	180
Db	121	CSVLFLTCISVHRVYLGICHPRLALRWGRPRLAGLLCLAVMLVWAGCLVPLNLFVYTSNKG	180
Qy	181	TTVLCHDTTRPEEFDHYVHFSSAVMGLLFGVPCILVTLCYGLMARRLYQPLPGSAQSSSR	240
Db	181	TTVLCHDTTRPEEFDHYVHFSSAVMGLLFGVPCILVTLCYGLMARRLYQPLPGSAQSSSR	240
Qy	241	LRSRLTIANVLTFAVCFVPHFTRITTYIARLEADCRVLNINVVYKVRPLASANS	300
Db	241	LRSRLTIANVLTFAVCFVPHFTRITTYIARLEADCRVLNINVVYKVRPLASANS	300
Qy	301	LDPVLVLLTGDKYRRQLRQLCGGKGPQPRTAASLALVSLPEDSSCWAATPDSSCSTP	360
Db	301	LDPVLVLLTGDKYRRQLRQLCGGKGPQPRTAASLALVSLPEDSSCWAATPDSSCSTP	360

Wed Apr 5 13:47:55 2006

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QY 361 RADRL 365
Db 361 RADRL 365

RESULT 2
US-11-127-877-46
; Sequence 46, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 46
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
-US-11-127-877-46

Query Match 33.0%; Score 641.5; DB 7; Length 373;
Best Local Similarity 40.0%; Pred. No. 1.2e-49;
Matches 140; Conservative 60; Mismatches 121; Indels 29; Gaps 9;

QY 17 GPGSS-----EVELDCWFDE-DFKFIPLPVSYAVVFLVGLGNAPTLWLFIFR 63
Db 20 GPGSSGNSIVASTAAVSSSFKCALTKTGFQFYLPVAVILVFLIIGFLGNSVAIMWVFH 79
64 LRPMDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKFVRFPLFYNLYCSV 123
80 MKPWSGISVYMFNLALADFLVLTLPALIFYFNKTDWIFGDAMCKLQRFIFHVNLYGSI 139
124 LFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLA--VWLTVAGCLVPLNFFVTTTS-NGK 180
140 LFLTCISAHRYSGVYPLKSL--GRKKNAICISVLVWLIYVVAISPILFYSGTGVKRN 197
181 TTVLCHDTRPEEFHDYVHFSSAVMGLLFGVPCLVTLVCYGLMARL-YQPLPGSAOSSS 239
198 KTIICYDTTSDYLSRYFIYSMCTTVAMFCVPLVILGCGLIVRALIYKOLD---NSPL 254
240 RLRSRTIAVLTVPFVAVCFVPHITRTIYYLARL---LEADCRVLNINVVYKVTPLAS 296
255 RKSIYLVIIIVTFVAVSYIPFHVWKTMLRLARLDFQTPAMCAFNDRVYATYQVTRGLAS 314
297 ANSCLDPVLYLTGDKYRQL-----ROLCGGKQPQRTAASSLALVSLPE 342
315 LNSCVDPILYFLAGDTFRRLSRATRKASRRSEANLQSKSEDMTLNILPE 364

QY 17 GPGSS-----EVELDCWFDE-DFKFIPLPVSYAVVFLVGLGNAPTLWLFIFR 63
Db 20 GPGSSGNSIVASTAAVSSSFKCALTKTGFQFYLPVAVILVFLIIGFLGNSVAIMWVFH 79
64 LRPMDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKFVRFPLFYNLYCSV 123
80 MKPWSGISVYMFNLALADFLVLTLPALIFYFNKTDWIFGDAMCKLQRFIFHVNLYGSI 139
124 LFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLA--VWLTVAGCLVPLNFFVTTTS-NGK 180
140 LFLTCISAHRYSGVYPLKSL--GRKKNAICISVLVWLIYVVAISPILFYSGTGVKRN 197
181 TTVLCHDTRPEEFHDYVHFSSAVMGLLFGVPCLVTLVCYGLMARL-YQPLPGSAOSSS 239
198 KTIICYDTTSDYLSRYFIYSMCTTVAMFCVPLVILGCGLIVRALIYKOLD---NSPL 254
240 RLRSRTIAVLTVPFVAVCFVPHITRTIYYLARL---LEADCRVLNINVVYKVTPLAS 296
255 RKSIYLVIIIVTFVAVSYIPFHVWKTMLRLARLDFQTPAMCAFNDRVYATYQVTRGLAS 314
297 ANSCLDPVLYLTGDKYRQL-----ROLCGGKQPQRTAASSLALVSLPE 342
315 LNSCVDPILYFLAGDTFRRLSRATRKASRRSEANLQSKSEDMTLNILPE 364

RESULT 3
US-11-222-874-6
; Sequence 6, Application US/11222874
; Publication No. US20060052329A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y1-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: LI0131 Foreign Countries
; CURRENT APPLICATION NUMBER: US/11/222,874
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/344,728
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/224,989
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; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-222-874-6

Query Match 33.0%; Score 641.5; DB 7; Length 373;
Best Local Similarity 40.0%; Pred. No. 1.2e-49;
Matches 140; Conservative 60; Mismatches 121; Indels 29; Gaps 9;

QY 17 GPGSS-----EVELDCWFDE-DFKFIPLPVSYAVVFLVGLGNAPTLWLFIFR 63
Db 20 GPGSSGNSIVASTAAVSSSFKCALTKTGFQFYLPVAVILVFLIIGFLGNSVAIMWVFH 79
64 LRPMDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKFVRFPLFYNLYCSV 123
80 MKPWSGISVYMFNLALADFLVLTLPALIFYFNKTDWIFGDAMCKLQRFIFHVNLYGSI 139
124 LFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLA--VWLTVAGCLVPLNFFVTTTS-NGK 180
140 LFLTCISAHRYSGVYPLKSL--GRKKNAICISVLVWLIYVVAISPILFYSGTGVKRN 197
181 TTVLCHDTRPEEFHDYVHFSSAVMGLLFGVPCLVTLVCYGLMARL-YQPLPGSAOSSS 239
198 KTIICYDTTSDYLSRYFIYSMCTTVAMFCVPLVILGCGLIVRALIYKOLD---NSPL 254
240 RLRSRTIAVLTVPFVAVCFVPHITRTIYYLARL---LEADCRVLNINVVYKVTPLAS 296
255 RKSIYLVIIIVTFVAVSYIPFHVWKTMLRLARLDFQTPAMCAFNDRVYATYQVTRGLAS 314
297 ANSCLDPVLYLTGDKYRQL-----ROLCGGKQPQRTAASSLALVSLPE 342
315 LNSCVDPILYFLAGDTFRRLSRATRKASRRSEANLQSKSEDMTLNILPE 364

RESULT 4
US-11-157-930-6
; Sequence 6, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-6

Query Match 26.5%; Score 515; DB 7; Length 367;
Best Local Similarity 36.0%; Pred. No. 2.1e-38;
Matches 126; Conservative 55; Mismatches 149; Indels 20; Gaps 9;

QY 3 STESLLRSLSGLSPGPG-----SSEVELDCWFDEDFKFIPLPVSYAVVFLVGLGNAPTL 57
Db 23 SDSSQSMNGLEVAP-PGLITNFSLATAPCCQSQETPLENMLFASFVLLDFILALVGNLAL 81
58 WLFIERLPWDATATYMFHALSDTLVLSLPTLIYYAAHNHPFGTEICKFVRFPLFYN 117
```

Db 82 WLFIRHSGTTPANVFLMHLAVADLSCLVLPVTRLVYHFGNHWPFGEIACRLTGFLFYL 141
Qy 118 NLYCSVLFLACISVHRVYGLCHPLRALRWGRPRLAGILCLAVMLVWAGCLVPLNLFVFTTS 177
Db 142 NMYASIFLACISADRELAIVHPVKSUKLRPLVYAHACAFVWVAVAVAPLLVSPQTV 201
Qy 178 NKGTVLCHDTTPPEEDHYHFSVAVMGLLFGVPCLVTLVYCYGLMARRLYQPLPGSAQS 237
Db 202 QTNHTVVCLQYR-EKASHALVSLAV---AFTFPFTTTCVLLIIRSLRQGL--RVEK 255
Qy 238 SSRLSRLRTTAVLVTPAVCFVPHITRTIYL-ARLLEADCRVLNVVYVKTVPRLAS 296
Db 256 RLTKAVKAVIAIYLAIFLVCFVPHYVNRVYVLYHSHGASCATORILALANRITSCLTS 315
Qy 297 ANSLDPLVLLTGDKYRROL-RQLCG---GKPK--QPTAASSLALVS 339
Db 316 LAGALDPIYFFVAEKRHALCNLLCGKRLKGPFPFEGKTNESSLSAKS 365

RESULT 5
US-11-222-874-2
; Sequence 2, Application US/11222874
; Publication No. US20060052329A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN P2YL-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: L10131 Foreign Countries
; CURRENT APPLICATION NUMBER: US/11/222,874
; PRIORITY FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/344,728
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/224,989
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-222-874-2

Query Match 26.4%; Score 514; DB 7; Length 337;
Best Local Similarity 35.1%; Pred. No. 2.3e-38;
Matches 101; Conservative 64; Mismatches 119; Indels 4; Gaps 2;
Qy 30 DED--FKELIPVSYAVVFLVGLGNAPTLWLFIFRLPWPDATATYMFHLALSDTLVYL 87
Db 26 DENIPLKMHLPVYIGIIFLVGFPGNAVVIISTYIFKMRPKSSTIIMLNACTOLLVLT 85
Qy 88 LPTLIYYAAHNPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRVYGLCHPLRALRW 147
Db 86 LPFLIHYASGENWIFGDMCKFRFSHFHNLVSIILPFTCFISFRYCVIHPMCSFSIH 145
Qy 148 RPLRAGLCLAVLWVAGCLVPLNLFVFTTSNKGTVLCHDTTRPEEDHYHFSVAVMGL 207
Db 146 KTRCAVACAVVWISLAVIPMTFLTSTNTRNSACLDTSDDELTKWYLIITAT 205
Qy 208 LFGVPCLVLYCYGLMARRLYQPLPGSAQSSRLSRISRTIAVLTVFAVCFVPHITRTI 267
Db 206 TFCFLPVLVITLCYTIITHTLTHGL--QTDSCCLKKARRLTLLLLAFVYCFPLPHILRVI 263
Qy 268 YILARLEADCRVLNVVYVKTVPRLASANSLDPLVLLTGDKYR 315
Db 264 RIESRLLSISCIENQIHEAVIVSRPLAALNTFGNLLLYVVSDFNQ 311

RESULT 6
US-11-157-930-4
; Sequence 4, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR

; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-4

Query Match 26.2%; Score 510; DB 7; Length 339;
Best Local Similarity 37.1%; Pred. No. 5.3e-38;
Matches 119; Conservative 52; Mismatches 136; Indels 14; Gaps 7;
Qy 27 CWFDEDFKILLPVSYAVVFLVGLGNAPTLWLFIFRLPWPDATATYMFHLALSDTLVYL 86
Db 23 CGQETPLENMLFASFLYLDLFIALVGVNTIALWLFIRDHKSGTPANVFLMHLAVADLSCLV 82
Qy 87 SLPTLIYYAAHNPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRVYGLCHPLRALRW 146
Db 83 VLPTRLVYHFGNHWPFGEIACRLTGFLFYWNLYASIFLACISADRELAIVHPVKSUKL 142
Qy 147 GRPLRAGLCLAVLWVAGCLVPLNLFVFTTSNKGTVLCHDTTRPEEDHYHFSVAVMGL 206
Db 143 RRLPYLAHLACAFVWVAVAVAPLLVSPQTVQTNHTVVCLQYR-EKASHALVSLAV-- 199
Qy 207 LLFGVPCLVLYCYGLMARRLYQPLPGSAQSSRLSRISRTIAVLTVFAVCFVPHITRT 266
Db 200 -AFTFPFTTTCVLLIIRSLRQGL--RVEKRLTKAVKAVIAIYLAIFLVCFVPHYVNR 256
Qy 267 IYIL-ARLLEADCRVLNVVYVKTVPRLASANSLDPLVLLTGDKYRROL-RQLCG-- 322
Db 257 VYVLYHSHGASCATORILALANRITSCLTSLNGALDPIYFFVAEKRHALCNLLCGKR 316
Qy 323 --GKPK--QPTAASSLALVS 339
Db 317 LKGPFPFEGKTNESSLSAKS 337

RESULT 7
US-11-072-175-145
; Sequence 145, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-145
Query Match 20.7%; Score 403; DB 7; Length 397;
Best Local Similarity 32.1%; Pred. No. 2.1e-28;

Matches		95; Conservative	57; Mismatches	124; Indels	20; Gaps	9;
QY	36	ILLPVSVAVVFLVGLGNAPTLWLFIFRLRPWDATATYMFHLALSDTLVLSLPTLIYY	95			
Db	76	VFLPIVITVIVVGLPSNGMALVFLFRKKHPAVIYMANLADALLSVINFLPKIAVH	135			
QY	96	AAHNHPFGTEICKFVRFLFYNNLYCSVFLTCTISVHYLGICHPRLALRWGRPRLAGLL	155			
Db	136	IHGNNIYGALCNVLIGFYGNMYSILFMTCLSVQRYWIVNPMGHSR-KKANIAIGI	194			
QY	156	CLAWLVVACCLVP-----NLFFVTSNKGTVLCHDTRPEEF---DHVHFSSAVMGL	207			
Db	195	SLAIWLLILVITPLVYVVKQTFIPALNITT---CHDVL-PEQLLVGDMFNFLSLAIG-	249			
QY	208	LFGVPCVLTVVCGLMARRLYQPLPGSAQSSRLSLRTIAVLTVFAVCFVFPFHITRTI	267			
Db	250	VFLFPAPLTASAVLIMRLRSSAMENSEKKRAIKLIVTVLWMLYLCFTPSNLLVV	309			
QY	268	YYLARLEADCRVLNVVNVYKVRPLASANSCLDPVLYLLTGDKYRRLQRLQ--LC	321			
Db	310	HYF--LJKSQGQ--SHVYALYIVALCLSTLNSCIDPVPYVYVSHDFRDHAKNALLC	361			
RESULT 8						
US-10-821-234-934						
; Sequence 934, Application US/10821234						
; Publication No. US20050255114A1						
; GENERAL INFORMATION:						
; APPLICANT: Labat, Ivan						
; APPLICANT: Stache-Grain, Birgit						
; APPLICANT: Andarmani, Susan						
; APPLICANT: Tang, Y. Tom						
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia						
; FILE REFERENCE: 821A						
; CURRENT APPLICATION NUMBER: US/10/821,234						
; PRIOR FILING DATE: 2004-04-07						
; PRIOR APPLICATION NUMBER: US 60/462,047						
; PRIOR FILING DATE: 2003-04-07						
; NUMBER OF SEQ ID NOS: 1704						
; SOFTWARE: Pct_seq_genes Version 1.0						
; SEQ ID NO 934						
; LENGTH: 485						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-821-234-934						
Query Match						
Best Local Similarity						
Matches						
20.4%; Score 397.5; DB 6; Length 485;						
; Sequence 934, Application US/10821234						
; Publication No. US20050255114A1						
; GENERAL INFORMATION:						
; APPLICANT: Labat, Ivan						
; APPLICANT: Stache-Grain, Birgit						
; APPLICANT: Andarmani, Susan						
; APPLICANT: Tang, Y. Tom						
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia						
; FILE REFERENCE: 821A						
; CURRENT APPLICATION NUMBER: US/10/821,234						
; PRIOR FILING DATE: 2004-04-07						
; PRIOR APPLICATION NUMBER: US 60/462,047						
; PRIOR FILING DATE: 2003-04-07						
; NUMBER OF SEQ ID NOS: 1704						
; SOFTWARE: Pct_seq_genes Version 1.0						
; SEQ ID NO 934						
; LENGTH: 485						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-821-234-934						
Query Match						
Best Local Similarity						
Matches						
97; Conservative						
60; Mismatches						
136; Indels						
31; Gaps						
QY	36	ILLPVSVAVVFLVGLGNAPTLWLFIFRLRPWDATATYMFHLALSDTLVLSLPTLIYY	95			
Db	163	LFVPSVYGVFVSVSLPNNIAIVFLIKMKVKKPAVYMLHLADVLVSVLPFKISY	222			
QY	96	AAHNHPFGTEICKFVRFLFYNNLYCSVFLTCTISVHYLGICHPRLALRWGRPRLAGLL	155			
Db	223	PSGDMQFSGELCFVTAFAFYCNVYASILLMTVISIDRFVAVYPMQSLNRTLGASFT	282			
QY	156	CLAWV-LVACGL-----VPLFFVTSNKGTVLCHDTRPEEF-HVHFSSA	203			
Db	283	CLAIWALAIAGVPLVLEQTIQVPLNITT-----CHDVNLNETLLEGYAYYFSA	333			
QY	204	VMGLFGVPCVLTVVCGLMARRLYQPLPGSAQSSRLSLRTIAVLTVFAVCFVFPFHI	263			
Db	334	FSAVFFFVPLIISTVCYVSIIRCLSS--SAVANRSKSRALFSLNFCIIFICFPINV	391			
QY	264	TRTIYY--LARLEADCRVLNVVNVYKVRPLASANSCLDPVLYLLTGDKYRRLQRLQ-L	320			
Db	392	LLIAHYSFLSHTSITEAYF-----AYLLCVSVSSICIDPLIYYVASSECQRYVYSIL	446			
QY	321	CGGKGPQPRTAASSLALVSLPDS	344			
Db	447	CKESSDPSYSSSQLMASKMDT	470			


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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-058-2

Query Match      19.3%; Score 375; DB 7; Length 415;
Best Local Similarity 30.6%; Pred. No. 6.7e-26;
Matches 114; Conservative 57; Mismatches 155; Indels 46; Gaps 11;

QY      6  SSLSRLSLGSPGSGSEVELDCW-----FDEDFKILLPVSYAVFVLGLGNAPTLW 58
DB      64  AALLENFSSSYDGENESDSCCTSPCPQDFSLNPDRAFLPALYSLLFLGLLGNAAV 123
QY      59  LIFRRLPMDATATYMFHLASDLYLVSPLTYIAAHNHPGTEICKFVRELFYWN 118
DB      124  VLLSRRTALSSDTDFLLHLAVADTLVLTLP--LMAVDAVQVFGSGCKVAGALFNIN 181
QY      119  LYCSVLFLATCISVHRVYLGICHPRLRWRGPRLAGLLCLAVMLVAVAGCLVPLNFFVTTSN 178
DB      182  FYAGALLACISPDRIYINIVHATQLYRGPAPRVTLTCLAVWGLCLLFPALPDFLSAH- 240
QY      179  KGTTVLCHD-----TRPEEFHYVHFSSAVMGLFG--VPCLVTLVYCYG-LMARLYQP 230
DB      241  -----HDERLNATHCQYNFPQVGRALTALRVQLVAGFLPLLVMAVCYAHILAVLLV-- 291
QY      231  LPSAQSRLRLSLRTIAVTLVFAVCFVPHITRIIYIARL--LEADCRVLNINVVY 288
DB      292  ---SRQRLRAMRLVWVWVAFALCWTPEYHLVLDVILMDIGALARNCGRESRVDVAK 347
QY      289  KVTPLASNSCLDPVLYLLTGDKYRQ-----LRQLCGGKQPQRTAASSLALVSLPED 343
DB      348  SVTSGLYGMYHCCLLPLLYAFVGVKFRMRMMLLLRLGCPNQRGLQRPSS-----RRD 401
QY      344  SSCRWAAATPODS 355
DB      402  SS--WSETSEAS, 411

Query Match      18.6%; Score 362.5; DB 6; Length 380;
Best Local Similarity 27.9%; Pred. No. 7.9e-25;
Matches 83; Conservative 56; Mismatches 100; Indels 59; Gaps 10;

QY      37  LLPVSYAVFVLGLGNAPTLWLFIFRLRPWDATATYMFHLASDLYLVSPLTYIY 94
DB      106  VIPAIYILLFVVGVPANIVTLWKLSLRTK---SISLVIHFTNLAIADLLFCVTLPKIAY 162
QY      95  YAAHNHPGTEICKFVRELFYWNLYCSVLFLTCISVHRVYLGICHPRLRWRGPRLAGL 154
DB      163  HLNGNWVFGVNCVCRITTVFYGNMYCAILLTOMGINRYLATATAHFTYQKLPKRSFSL 222
QY      155  LCLAVMLVAVAGCLVPLNFFVTTSNK-----GTVLCHDIT--RPEEPHYVHFSSAVM 205
DB      223  MCGWVWVWVFLYMLP---FVLKQYHLVHSEITTCDDVVDVACESPSSFRFYFVSLAFF 279
QY      206  GLLFGVPCVTLVYCYGLMARRLYQPLPGSAQSSR--LRSRLTIAVTLVFAVCFV-- 260
DB      280  GFL--IPFVIIIPCYTTLIHL-----KSKDRWLGVYKAVALLILVIFTICFAPNI 329
QY      261  -----FHLTRIYILARLEADCRVLNINVVYKVTPLASNSCLDPVLYLL 308
DB      330  ILVIHHANYYYHNTDSLIFM-----YLIACLGSLNSCLDPFLYFV 370

Query Match      18.9%; Score 367; DB 7; Length 357;
Best Local Similarity 29.8%; Pred. No. 2.9e-25;
Matches 86; Conservative 67; Mismatches 116; Indels 20; Gaps 7;

US-11-261-135-2

Query Match      18.6%; Score 362.5; DB 6; Length 380;
Best Local Similarity 27.9%; Pred. No. 7.9e-25;
Matches 83; Conservative 56; Mismatches 100; Indels 59; Gaps 10;

QY      37  LLPVSYAVFVLGLGNAPTLWLFIFRLRPWDATATYMFHLASDLYLVSPLTYIY 94
DB      106  VIPAIYILLFVVGVPANIVTLWKLSLRTK---SISLVIHFTNLAIADLLFCVTLPKIAY 162
QY      95  YAAHNHPGTEICKFVRELFYWNLYCSVLFLTCISVHRVYLGICHPRLRWRGPRLAGL 154
DB      163  HLNGNWVFGVNCVCRITTVFYGNMYCAILLTOMGINRYLATATAHFTYQKLPKRSFSL 222
QY      155  LCLAVMLVAVAGCLVPLNFFVTTSNK-----GTVLCHDIT--RPEEPHYVHFSSAVM 205
DB      223  MCGWVWVWVFLYMLP---FVLKQYHLVHSEITTCDDVVDVACESPSSFRFYFVSLAFF 279
QY      206  GLLFGVPCVTLVYCYGLMARRLYQPLPGSAQSSR--LRSRLTIAVTLVFAVCFV-- 260
DB      280  GFL--IPFVIIIPCYTTLIHL-----KSKDRWLGVYKAVALLILVIFTICFAPNI 329
QY      261  -----FHLTRIYILARLEADCRVLNINVVYKVTPLASNSCLDPVLYLL 308
DB      330  ILVIHHANYYYHNTDSLIFM-----YLIACLGSLNSCLDPFLYFV 370

Search completed: April 4, 2006, 20:29:49
Job time : 26 secs
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GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 20:25:38 ; Search time 167 seconds
(without alignments)
913.220 Million cell updates/sec

Title: US-10-811-198-2

Perfect score: 1944

Sequence: 1 MASTESSLLRSLGSLPGSGS.....CRWAATPDSSCTPRADRL 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*Result No.	Score	Match	Length	DB ID	Description
1	1944	100.0	365	3	US-09-745-842-16
2	1944	100.0	365	4	US-10-225-567A-332
3	1944	100.0	365	4	US-10-753-695-2
4	1944	100.0	365	5	US-10-811-198-2
5	1944	100.0	365	5	US-10-811-192-2
6	1940	99.8	365	4	US-09-077-173A-2
7	1932	99.4	365	4	US-10-366-288-42
8	1597	82.2	361	3	US-09-964-821B-15
9	1597	82.2	361	4	US-10-010-568-9
10	1597	82.2	361	4	US-10-268-332-15
11	1597	82.2	361	4	US-10-375-157-9
12	1597	82.2	361	4	US-10-072-012-521
13	1597	82.2	361	4	US-10-775-965-15
14	1127.5	58.0	374	3	US-09-745-842-15
15	1127.5	58.0	374	4	US-10-010-568-11
16	1127.5	58.0	374	4	US-10-375-157-11
17	1127.5	58.0	374	4	US-10-072-012-518
18	1007.5	51.8	537	4	US-10-311-956-4
19	1007.5	51.8	537	4	US-10-010-568-12
20	1007.5	51.8	537	4	US-10-375-157-12
21	1007.5	51.8	537	4	US-10-055-569A-52
22	1007.5	51.8	537	4	US-10-072-012-517
23	965	49.6	377	3	US-09-745-842-17
24	965	49.6	377	4	US-10-225-567A-217
25	965	49.6	377	5	US-10-756-149-5688
26	955	49.1	374	4	US-10-242-499-3
27	951	48.9	341	4	US-10-270-567-3

28	950	48.9	374	4	US-10-010-568-13	Sequence 13, Appl
29	950	48.9	374	4	US-10-375-157-13	Sequence 13, Appl
30	934	48.0	375	3	US-09-947-922-3	Sequence 3, Appl
31	934	48.0	375	4	US-10-706-532-3	Sequence 3, Appl
32	641.5	33.0	373	3	US-09-745-842-14	Sequence 14, Appl
33	641.5	33.0	373	4	US-10-092-135-6	Sequence 6, Appl
34	641.5	33.0	373	4	US-10-225-567A-219	Sequence 219, Appl
35	641.5	33.0	373	4	US-10-010-568-8	Sequence 8, Appl
36	641.5	33.0	373	4	US-10-375-157-8	Sequence 8, Appl
37	641.5	33.0	373	4	US-10-023-634-59	Sequence 59, Appl
38	641.5	33.0	373	4	US-10-055-569A-51	Sequence 51, Appl
39	641.5	33.0	373	4	US-10-344-728-6	Sequence 6, Appl
40	641.5	33.0	373	6	US-11-063-894-6	Sequence 6, Appl
41	631	32.5	362	3	US-09-991-225-4	Sequence 4, Appl
42	631	32.5	362	4	US-10-092-135-4	Sequence 4, Appl
43	631	32.5	362	4	US-10-010-568-4	Sequence 4, Appl
44	631	32.5	362	4	US-10-044-643-47	Sequence 47, Appl
45	631	32.5	362	4	US-10-369-405-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-745-842-16

Sequence 16, Application US/09745842

Publication No. US2003010777A1

GENERAL INFORMATION:

APPLICANT: Conley, Pamela B.

APPLICANT: Jantzen, Hans-Michael

APPLICANT: Ramakrishnan-DuBridge, Vanitha

APPLICANT: Julius, David

APPLICANT: Hollopetter, Gunter

APPLICANT: COR Therapeutics, Inc.

TITLE OF INVENTION: P2Y12 Receptor

FILE REFERENCE: 44481-5053-US

CURRENT APPLICATION NUMBER: US/09/745,842

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: US 60/171,622

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 365

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: P2Y4 pyrimidinergic receptor

US-09-745-842-16

Query Match 100.0%; Score 1944; DB 3; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.3e-158;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASTESSLLRSLGSLPGSGSVELDCWDFDEKFKILLPVSYAVFVLGLNAPTLMWF	60
Db	1	MASTESSLLRSLGSLPGSGSVELDCWDFDEKFKILLPVSYAVFVLGLNAPTLMWF	60
Qy	61	IFRLRPWDATATYMEHLASDLYLVSLPTLYYYAAHNNHPFGTEICKFVRFIFYWNL	120
Db	61	IFRLRPWDATATYMEHLASDLYLVSLPTLYYYAAHNNHPFGTEICKFVRFIFYWNL	120
Qy	121	CSVLFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG	180
Db	121	CSVLFLTCISVHRYLGIChPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG	180
Qy	181	TTVLCHDTRPEFDHYVHFSSAVMGLLFGVPCVLTVLCYGLMARRLYQPLPQAQSSSR	240
Db	181	TTVLCHDTRPEFDHYVHFSSAVMGLLFGVPCVLTVLCYGLMARRLYQPLPQAQSSSR	240
Qy	241	LRSLRTIANVLTVFAVCFVPEHITRTIYLLARLEADCRVLNIWVYKVTPLASANS	300
Db	241	LRSLRTIANVLTVFAVCFVPEHITRTIYLLARLEADCRVLNIWVYKVTPLASANS	300

us-10-811-198-2.rapbm

Wed Apr 5 13:47:54 2006

301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
361 RADRL 365
361 RADRL 365
RESULT 2
US-10-225-567A-332
Sequence 332, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Christine L.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 332
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-332
Query Match 100.0%; Score 1944; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-158;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASTESSLLRSLGSLPGSGSSEVELDCWFDEDFKFIILLPVSYAVVVLGGLNAPTLLWLF 60
Db 1 MASTESSLLRSLGSLPGSGSSEVELDCWFDEDFKFIILLPVSYAVVVLGGLNAPTLLWLF 60
QY 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLEFYNLY 120
Db 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLEFYNLY 120
QY 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVMLVAGCLVPNLFFVTTSNKG 180
Db 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVMLVAGCLVPNLFFVTTSNKG 180
QY 181 TTVLCHDTRPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
QY 241 LRSRTIAVLTAVFVAVCFVPHITRTIYYLARLLEADCRVLNVVYKTRPLASANS 300
Db 241 LRSRTIAVLTAVFVAVCFVPHITRTIYYLARLLEADCRVLNVVYKTRPLASANS 300
QY 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
Db 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
361 RADRL 365
361 RADRL 365
RESULT 3
US-10-753-695-2
Sequence 2, Application US/10753695
Publication No. US20040175766A1
GENERAL INFORMATION:
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
TITLE OF INVENTION: P2Y4 Antibody and Methods of Use
FILE REFERENCE: 9409/2113B
CURRENT APPLICATION NUMBER: US/10/811,198
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: 10/753,695
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: 09/077,173
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/BE96/00123
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: EP 95870124.5

APPLICANT: Piroton, Sabine
APPLICANT: Piroton, Sabine
TITLE OF INVENTION: Human Pyrimidine Receptor
FILE REFERENCE: 9409/2113
CURRENT APPLICATION NUMBER: US/10/753,695
CURRENT FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: 09/077,173
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/BE96/00123
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: EP 95870124.5
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-10-753-695-2
Query Match 100.0%; Score 1944; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-158;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASTESSLLRSLGSLPGSGSSEVELDCWFDEDFKFIILLPVSYAVVVLGGLNAPTLLWLF 60
Db 1 MASTESSLLRSLGSLPGSGSSEVELDCWFDEDFKFIILLPVSYAVVVLGGLNAPTLLWLF 60
QY 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLEFYNLY 120
Db 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLEFYNLY 120
QY 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVMLVAGCLVPNLFFVTTSNKG 180
Db 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVMLVAGCLVPNLFFVTTSNKG 180
QY 181 TTVLCHDTRPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEDHYVHSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
QY 241 LRSRTIAVLTAVFVAVCFVPHITRTIYYLARLLEADCRVLNVVYKTRPLASANS 300
Db 241 LRSRTIAVLTAVFVAVCFVPHITRTIYYLARLLEADCRVLNVVYKTRPLASANS 300
QY 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
Db 301 LDPVLYLLTGDKYRQLRQLCGGKQPQRTAASSLALVSLPEDSSCRWAATPDQSSCSTP 360
361 RADRL 365
361 RADRL 365
RESULT 4
US-10-811-198-2
Sequence 2, Application US/10811198
Publication No. US20040259171A1
GENERAL INFORMATION:
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
APPLICANT: Boeynaems, Jean-Marie
TITLE OF INVENTION: P2Y4 Antibody and Methods of Use
FILE REFERENCE: 9409/2113B
CURRENT APPLICATION NUMBER: US/10/811,198
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: 10/753,695
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: 09/077,173
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/BE96/00123
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: EP 95870124.5

;; PRIOR FILING DATE: 1995-11-21
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 365
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-811-198-2

Query Match 100.0%; Score 1944; DB 5; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-158;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
QY 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
DB 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
QY 121 CSVLFLTCISVHYRIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVNLFPFVTTSNKG 180
DB 121 CSVLFLTCISVHYRIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVNLFPFVTTSNKG 180
QY 181 TTVLCHDTRPEEFHYHFFSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240
DB 181 TTVLCHDTRPEEFHYHFFSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240
QY 241 LRSLEIAVLTVFAVCFVPHITRTIYLLARLLEADCRVLNVVYKVTPLASANS 300
DB 241 LRSLEIAVLTVFAVCFVPHITRTIYLLARLLEADCRVLNVVYKVTPLASANS 300
QY 301 LDPVLYLTGDKYRQLRQLCGGKQPRTAAASSLALVSLPDDSSCRWAATPDSSCSTP 360
DB 301 LDPVLYLTGDKYRQLRQLCGGKQPRTAAASSLALVSLPDDSSCRWAATPDSSCSTP 360
QY 361 RADRL 365
DB 361 RADRL 365

RESULT 5

-US-10-811-192-2
; Sequence 2, Application US/10811192
; Publication No. US20040268426A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; APPLICANT: Boeynaems, Jean-Marie
; APPLICANT: Pitotton, Sabine
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: P2Y4 receptor transgenic and knockout non-human mammals
; FILE REFERENCE: 9409/2113C
; CURRENT APPLICATION NUMBER: US/10/811,192
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 10/753,695
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 09/077,173
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/BE96/00123
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: EP 95870124.5
; PRIOR FILING DATE: 1995-11-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-192-2

Query Match 100.0%; Score 1944; DB 5; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-158;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
QY 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
DB 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
QY 121 CSVLFLTCISVHYRIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVNLFPFVTTSNKG 180
DB 121 CSVLFLTCISVHYRIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVNLFPFVTTSNKG 180
QY 181 TTVLCHDTRPEEFHYHFFSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240
DB 181 TTVLCHDTRPEEFHYHFFSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240
QY 241 LRSLEIAVLTVFAVCFVPHITRTIYLLARLLEADCRVLNVVYKVTPLASANS 300
DB 241 LRSLEIAVLTVFAVCFVPHITRTIYLLARLLEADCRVLNVVYKVTPLASANS 300
QY 301 LDPVLYLTGDKYRQLRQLCGGKQPRTAAASSLALVSLPDDSSCRWAATPDSSCSTP 360
DB 301 LDPVLYLTGDKYRQLRQLCGGKQPRTAAASSLALVSLPDDSSCRWAATPDSSCSTP 360
QY 361 RADRL 365
DB 361 RADRL 365

RESULT 6

US-09-077-173A-2
; Sequence 2, Application US/09077173A
; Publication No. US20030082674A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,173A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/BE 96/00123
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-173A-2

Query Match 99.8%; Score 1940; DB 3; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.8e-158;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLGNAPTLLWF 60
QY 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
DB 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGTEICKFVRFLLFYNNLY 120
QY 121 CSVLFLTCISVHYRIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVNLFPFVTTSNKG 180

Db 121 CSVLFTCTSVHRYLGI CHPLRALRWGRPRLAGLLCLAVLWVAVAGCLVPLNLFVFTTSNGK 180
Qy 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240
Qy 241 LRSRTIAVLTAVFCVFPFHITRTIYLLARLEADCRVLNIVNVVYKVRPLASANS 300
Db 241 LRSRTIAVLTAVFCVFPFHITRTIYLLARLEADCRVLNIVNVVYKVRPLASANS 300
Qy 301 LDPVLYLTGDKYRRQLRQLCGGKQPQRTAASSLALVSLPDSRCRWAATPDSSCSTP 360
Db 301 LDPVLYLTGDKYRRQLRQLCGGKQPQRTAASSLALVSLPDSRCRWAATPDSSCSTP 360
Qy 361 RADRL 364
Db 361 RADRL 364

RESULT 7
US-10-366-288-42
; Sequence 42, Application US/10366288
; Publication No. US20030216288A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas
; APPLICANT: Weich, Nadine S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,
; TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 12825, 9952, 5816,
; TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
; TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
; FILE REFERENCE: MPI02-025PIRNOVIN
; CURRENT APPLICATION NUMBER: US/10/366,288
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/357,391
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/380,249
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/391,306
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/406,297
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/412,007
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/417,508
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/432,318
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-366-288-42

Query Match 99.4%; Score 1932; DB 4; Length 365;
Best Local Similarity 99.2%; Pred. No. 1.4e-157;
Matches 362; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLNAPTLLWF 60
Db 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLNAPTLLWF 60
Qy 61 IFRLRPMDATATYMFHLASDTLYVLSPLTIYLYAAHNPFGTEICKFVRFLFYNNLY 120
Db 61 IFRLRPMDATATYMFHLASDTLYVLSPLTIYLYAAHNPFGTEICKFVRFLFYNNLY 120
Qy 121 CSVLFTCTSVHRYLGI CHPLRALRWGRPRLAGLLCLAVLWVAVAGCLVPLNLFVFTTSNGK 180
Db 121 CSVLFTCTSVHRYLGI CHPLRALRWGRPRLAGLLCLAVLWVAVAGCLVPLNLFVFTTSNGK 180
Qy 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240

Db 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240
Qy 241 LRSRTIAVLTAVFCVFPFHITRTIYLLARLEADCRVLNIVNVVYKVRPLASANS 300
Db 241 LRSRTIAVLTAVFCVFPFHITRTIYLLARLEADCRVLNIVNVVYKVRPLASANS 300
Qy 301 LDPVLYLTGDKYRRQLRQLCGGKQPQRTAASSLALVSLPDSRCRWAATPDSSCSTP 360
Db 301 LDPVLYLTGDKYRRQLRQLCGGKQPQRTAASSLALVSLPDSRCRWAATPDSSCSTP 360
Qy 361 RADRL 365
Db 361 RADRL 365

RESULT 8
US-09-964-821B-15
; Sequence 15, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: PEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M. G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY3,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042NP
; CURRENT APPLICATION NUMBER: US/09/964,821B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,783
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,171
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 361
; TYPE: PRT
; ORGANISM: RAT
US-09-964-821B-15

Query Match 82.2%; Score 1597; DB 3; Length 361;
Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;
Qy 1 MASTESSLLRSLGSLPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLNAPTLLWF 60
Db 1 MASTESSLLRSLGSLPGSGSGDG----DCRFNEEFKILLPMSYAVVVLGLNAPTLLWF 56
Qy 61 IFRLRPMDATATYMFHLASDTLYVLSPLTIYLYAAHNPFGTEICKFVRFLFYNNLY 120
Db 57 LFRLRPMDATATYMFHLASDTLYVLSPLTIYLYAAHNPFGTEICKFVRFLFYNNLY 116
Qy 121 CSVLFTCTSVHRYLGI CHPLRALRWGRPRLAGLLCLAVLWVAVAGCLVPLNLFVFTTSNGK 180
Db 117 CSVLFTCTSVHRYLGI CHPLRALRWGRPRFASLLCLGWLWVAVAGCLVPLNLFVFTTSNGK 176
Qy 181 TTVLCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240
Db 177 TTILCHDTRPEEFHYHFFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 236
Qy 241 LRSRTIAVLTAVFCVFPFHITRTIYLLARLEADCRVLNIVNVVYKVRPLASANS 300
Db 237 LRSRTIAVLTAVFCVFPFHITRTIYQARLLQADCHVLNIVNVVYKVRPLASANS 296

QY 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAAASSLALVSLPEDSSCRWAATPDSSCSTP 360
|||
Db 297 LDPVLYLFTGDKYRNQLQQLCRGSKPKRPTAAASSLALVTLHEESISRWADTHQDSTFSAY 356
|||
QY 361 RADRL 365
|||
Db 357 EGDRL 361

RESULT 9

US-10-010-568-9
; Sequence 9, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY23, EXPRESSED HI
; FILE REFERENCE: D0077A CIP
; CURRENT APPLICATION NUMBER: US/10/010,568
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/269,795
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 361
; TYPE: PRT
; ORGANISM: RATTUS NORVEGICUS
US-10-010-568-9

Query Match 82.2%; Score 1597; DB 4; Length 361;

Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKFIILLPVSYAVVFLGLGNAPTLMWF 60
|||
Db 1 MTSAESLLFTSLGSPSSGDG----DCRFNEEFKFIILLPMSYAVVFLGLGNAPTLMWF 56
|||
QY 61 IFRLRPMDATATYMFHLALSDTLVLSLPTLIYYAAAHNHPFGTEICKFVRFLFYNNLY 120
|||
Db 57 LFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAAHNHPFGTEICKFVRFLFYNNLY 116
|||
QY 121 CSVLFLTCISVHRYLGICHPRLRWGRPRRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
|||
Db 117 CSVLFLTCISVHRYLGICHPRLRWGRPRFASLLCLGWLWVAGCLVPLNFFVTTNANG 176
|||
QY 181 TTVLCHDTTRPEEDHYHVFSSAVMGLLFGVPCLVTLVLCYGLMARLLYQPLPGSAOSSSR 240
|||
Db 177 TTILCHDTTLPEEDHYHVFSSAVMGLLFGVPCLVTLVLCYGLMARLLYRPLPGAGQSSSR 236
|||
QY 241 LRSRLTIAVLTVFVAVCFVPHITRTIYYLARLEADCRVLNINVVYKVRPLASANSNC 300
|||
Db 237 LRSRLTIAVLTVFVAVCFVPHITRTIYYQARLLQADCHVLNINVVYKVRPLASANSNC 296
|||
QY 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAAASSLALVSLPEDSSCRWAATPDSSCSTP 360
|||
Db 297 LDPVLYLFTGDKYRNQLQQLCRGSKPKRPTAAASSLALVTLHEESISRWADTHQDSTFSAY 356
|||
QY 361 RADRL 365
|||
Db 357 EGDRL 361

RESULT 10

US-10-268-332-15
; Sequence 15, Application US/10268332
; Publication No. US2003015748A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY3, EXPRESSED HIGH
; FILE REFERENCE: D0077A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 10/010,568
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/269,795
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2

FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Rat
US-10-268-332-15

Query Match 82.2%; Score 1597; DB 4; Length 361;

Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKFIILLPVSYAVVFLGLGNAPTLMWF 60
|||
Db 1 MTSAESLLFTSLGSPSSGDG----DCRFNEEFKFIILLPMSYAVVFLGLGNAPTLMWF 56
|||
QY 61 IFRLRPMDATATYMFHLALSDTLVLSLPTLIYYAAAHNHPFGTEICKFVRFLFYNNLY 120
|||
Db 57 LFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAAHNHPFGTEICKFVRFLFYNNLY 116
|||
QY 121 CSVLFLTCISVHRYLGICHPRLRWGRPRRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
|||
Db 117 CSVLFLTCISVHRYLGICHPRLRWGRPRFASLLCLGWLWVAGCLVPLNFFVTTNANG 176
|||
QY 181 TTVLCHDTTRPEEDHYHVFSSAVMGLLFGVPCLVTLVLCYGLMARLLYQPLPGSAOSSSR 240
|||
Db 177 TTILCHDTTLPEEDHYHVFSSAVMGLLFGVPCLVTLVLCYGLMARLLYRPLPGAGQSSSR 236
|||
QY 241 LRSRLTIAVLTVFVAVCFVPHITRTIYYLARLEADCRVLNINVVYKVRPLASANSNC 300
|||
Db 237 LRSRLTIAVLTVFVAVCFVPHITRTIYYQARLLQADCHVLNINVVYKVRPLASANSNC 296
|||
QY 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAAASSLALVSLPEDSSCRWAATPDSSCSTP 360
|||
Db 297 LDPVLYLFTGDKYRNQLQQLCRGSKPKRPTAAASSLALVTLHEESISRWADTHQDSTFSAY 356
|||
QY 361 RADRL 365
|||
Db 357 EGDRL 361

RESULT 11

US-10-375-157-9
; Sequence 9, Application US/10375157
; Publication No. US20030224458A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY23, EXPRESSED
; FILE REFERENCE: D0077A CIP
; CURRENT APPLICATION NUMBER: US/10/375,157
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 10/010,568
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/269,795
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2


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; SEQ ID NO 9
; LENGTH: 361
; TYPE: PRT
; ORGANISM: RATTUS NORVEGICUS
US-10-375-157-9

Query Match      82.2%; Score 1597; DB 4; Length 361;
Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

1 MASTESLLRSLGSLGSPGSSSEVELDCWDEDFKILLPVSYAVVVLGLNAPTLLWLF 60
1 MTSAESLLFTSLGSPSSGSGD-----DCRFNEEFKILLPMSYAVVVLGLNAPTLLWLF 56
61 IFLRPMWDATATYMFHLASDITLYVLSPLTLYVYAAHNPFGTEICKFVRFYWNLY 120
57 LFLRPMWDATATYMFHLASDITLYVLSPLTLYVYAAHNPFGTEICKFVRFYWNLY 116
121 CSVLFTLCISVHRYLGICHPRLRWRGRPRFASLLCLGWLWVAGCLVPLNFFVTTNKG 180
117 CSVLFTLCISVHRYLGICHPRLRWRGRPRFASLLCLGWLWVAGCLVPLNFFVTTNANG 176
181 TTVLCHDTRPEEPFDHYVFFSSAVMGLLFGVPCILVTVCYGLMARRLYQPLPGSQSSSR 240
177 TTVLCHDTRPEEPFDHYVFFSSAVMGLLFGVPCILVTVCYGLMARRLYQPLPGSQSSSR 236
241 LRSRTIAVLTVPFVAVCFVPHITRTIYLLARLLEADCRVLNINVVYKVTPLASANSC 300
237 LRSRTIAVLTVPFVAVCFVPHITRTIYLLARLLEADCRVLNINVVYKVTPLASANSC 296
301 LDPVLYLLTGDYKRRQLRQLCGGKQPQRTAASSLALVSLPDSRCWAATPQSSCSTP 360
297 LDPVLYLLTGDYKRRQLRQLCGGKQPQRTAASSLALVSLPDSRCWAATPQSSCSTP 356
361 RADRL 365
357 EGDR 361

RESULT 13
US-10-775-965-15
Sequence 15, Application US/10775965
Publication No. US20040209808A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Kornacker, Michael
TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: D0286 NP
CURRENT APPLICATION NUMBER: US/10/775,965
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: U.S. 60/446,655
PRIOR FILING DATE: 2003-02-11

; SEQ ID NO 9
; LENGTH: 361
; TYPE: PRT
; ORGANISM: RATTUS NORVEGICUS
US-10-375-157-9

Query Match      82.2%; Score 1597; DB 4; Length 361;
Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

1 MASTESLLRSLGSLGSPGSSSEVELDCWDEDFKILLPVSYAVVVLGLNAPTLLWLF 60
1 MTSAESLLFTSLGSPSSGSGD-----DCRFNEEFKILLPMSYAVVVLGLNAPTLLWLF 56
61 IFLRPMWDATATYMFHLASDITLYVLSPLTLYVYAAHNPFGTEICKFVRFYWNLY 120
57 LFLRPMWDATATYMFHLASDITLYVLSPLTLYVYAAHNPFGTEICKFVRFYWNLY 116
121 CSVLFTLCISVHRYLGICHPRLRWRGRPRFASLLCLGWLWVAGCLVPLNFFVTTNKG 180
117 CSVLFTLCISVHRYLGICHPRLRWRGRPRFASLLCLGWLWVAGCLVPLNFFVTTNANG 176
181 TTVLCHDTRPEEPFDHYVFFSSAVMGLLFGVPCILVTVCYGLMARRLYQPLPGSQSSSR 240
177 TTVLCHDTRPEEPFDHYVFFSSAVMGLLFGVPCILVTVCYGLMARRLYQPLPGSQSSSR 236
241 LRSRTIAVLTVPFVAVCFVPHITRTIYLLARLLEADCRVLNINVVYKVTPLASANSC 300
237 LRSRTIAVLTVPFVAVCFVPHITRTIYLLARLLEADCRVLNINVVYKVTPLASANSC 296
301 LDPVLYLLTGDYKRRQLRQLCGGKQPQRTAASSLALVSLPDSRCWAATPQSSCSTP 360
297 LDPVLYLLTGDYKRRQLRQLCGGKQPQRTAASSLALVSLPDSRCWAATPQSSCSTP 356
361 RADRL 365
357 EGDR 361

RESULT 12
US-10-072-012-521
Sequence 521, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A.
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
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; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 361
; TYPE: PRT
; ORGANISM: rat
US-10-775-965-15

Query Match
  82.2%; Score 1597; DB 4; Length 361;
Best Local Similarity 82.7%; Pred. No. 8.1e-129;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

Qy 1 MASTESSLRSLGSLGSPGSSSEVELDCWFDEDFKILLPVSAVVFVLGLGNAPTLMWF 60
Db 1 MTSAESLPTSLGSPSSGDG----DCRFNEEFKILLPMSYAVVFVLGLGNAPTLMWF 56

Qy 61 IFRLRPMDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGTEICKFVRFYFNLY 120
Db 57 LFRLRPMDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGTGLCKFVRFYFNLY 116

Qy 121 CSVLFLTCISVHRVYLGICHPRLRWGRPRLAGLCLAVLWVAGCLVPLNLFVTTNSKG 180
Db 117 CSVLFLTCISVHRVYLGICHPRLRWGRPRFASLLCLGVLWVAGCLVPLNLFVTTNANG 176

Qy 181 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYOPLPGSAQSSSR 240
Db 177 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYOPLPGSAQSSSR 236

Qy 241 LRSRLTIAVLTAVFVAVCFVPHITRTIYYLARLEADCRVLNINVVVYKVRPLASANS 300
Db 237 LRSRLTIAVLTAVFVAVCFVPHITRTIYYQARLLQADCHVLNINVVVYKVRPLASANS 296

Qy 301 LDPVLYLTGDKYRRLQOLCGGKQPQRTAASSIALVSLPDESSCRWAATPQSSSCTP 360
Db 297 LDPVLYLTGDKYRRLQOLCGGKQPQRTAASSIALVSLPDESSISRWADTHODSTFSAY 356

Qy 361 RADRL 365
Db 357 EGDRL 361

RESULT 14
US-09-745-842-15
; Sequence 15, Application US/09745842
; Publication No. US2003017077A1
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopeter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; FEATURES:
; OTHER INFORMATION: Turkey p2Y nucleotide receptor; tp2ynovel
US-09-745-842-15

Query Match
  58.0%; Score 1127.5; DB 3; Length 374;
Best Local Similarity 59.3%; Pred. No. 1.8e-88;
Matches 208; Conservative 56; Mismatches 70; Indels 17; Gaps 4;

Qy 9 LRSGLSP-----GPGSSEVELDCWFDEDFKILLPVSAVVFVLGLGNAPTLM 58
Db 5 VRMFSLAPWPTPTPWLGGNTTAAAEAKCVNEEFKILLPISYGVVFGVGLPLNSWAMW 64

Qy 59 LFIPLRPMDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGTEICKFVRFYFN 118
Db 65 IFVSRMRPNWNTTMYMFLAISDTLYVLSLPTLIYYAADRNWPFKGVCKIVRFLFYAN 124

Qy 119 LYCSVLFLTCISVHRVYLGICHPRLRWGRPRLAGLCLAVLWVAGCLVPLNLFVTTNS 178
Db 125 LYSSILFLTCISVHRVYLGICHPIRSKWVKTKARLICVGVWLVVTTICLIPNLFVTTSS 184

Qy 179 KGTIVLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYO---PLPSA 235
Db 185 KONSTLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYO---PLPSA 244

Qy 236 QSSRLRSLRTIAVLTAVFVAVCFVPHITRTIYYLARLEADCRVLNINVVVYKVRPLA 295
Db 245 VPSYKRSIKMIIIVLTAVFAICFVPHITRTIYYTSRYFOADCOTLNIINFTYKTRPLA 304

Qy 296 SANSCLDPVLYLTGDKYRRLQOLCGGKQPQRTAASS-LALVSLPEDSS 345
Db 305 SINSCLDPVLYLTGDKYRRLQOLCGGKQPQRTAASS-LALVSLPEDSS 352

Query Match
  58.0%; Score 1127.5; DB 4; Length 374;
Best Local Similarity 59.3%; Pred. No. 1.8e-88;
Matches 208; Conservative 56; Mismatches 70; Indels 17; Gaps 4;

Qy 9 LRSGLSP-----GPGSSEVELDCWFDEDFKILLPVSAVVFVLGLGNAPTLM 58
Db 5 VRMFSLAPWPTPTPWLGGNTTAAAEAKCVNEEFKILLPISYGVVFGVGLPLNSWAMW 64

Qy 59 LFIPLRPMDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGTEICKFVRFYFN 118
Db 65 IFVSRMRPNWNTTMYMFLAISDTLYVLSLPTLIYYAADRNWPFKGVCKIVRFLFYAN 124

Qy 119 LYCSVLFLTCISVHRVYLGICHPRLRWGRPRLAGLCLAVLWVAGCLVPLNLFVTTNS 178
Db 125 LYSSILFLTCISVHRVYLGICHPIRSKWVKTKARLICVGVWLVVTTICLIPNLFVTTSS 184

Qy 179 KGTIVLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYO---PLPSA 235
Db 185 KONSTLCHDTRPEEFHYVHFSSAVMGLLFGVPCVLTLYCYGLMARRLYO---PLPSA 244

Qy 236 QSSRLRSLRTIAVLTAVFVAVCFVPHITRTIYYLARLEADCRVLNINVVVYKVRPLA 295
Db 245 VPSYKRSIKMIIIVLTAVFAICFVPHITRTIYYTSRYFOADCOTLNIINFTYKTRPLA 304

Qy 296 SANSCLDPVLYLTGDKYRRLQOLCGGKQPQRTAASS-LALVSLPEDSS 345
Db 305 SINSCLDPVLYLTGDKYRRLQOLCGGKQPQRTAASS-LALVSLPEDSS 352
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us-10-811-198-2.rapbm

Wed Apr 5 13:47:54 2006

Db 305 SINSCLDPILYFMAGDKYRGELRR---GAAQRPVPVPTSLIALVSPVDSS 352

Search completed: April 4, 2006, 20:29:19
Job time : 168 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2006, 20:06:42 ; Search time 189 Seconds
(without alignments)
848.536 Million cell updates/sec

Title: US-10-811-198-2

Perfect score: 1944

Sequence: 1 MASTESLLRLSLGLSPGPGS.....CRWAATPQDSCTPRADRL 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1944	100.0	365	2 AAW23606	Aaw23606 Human P2Y
2	1944	100.0	365	4 AAE04391	Aae04391 Human P2Y
3	1944	100.0	365	6 ABP81923	Abp81923 Human P2Y
4	1944	100.0	365	8 ADO29598	Ado29598 Human GPC
5	1944	100.0	365	8 ADP49193	Adp49193 Human P2Y
6	1932	99.4	365	7 ADE04063	Ade04063 Human P2Y
7	1533.5	85.1	316	8 ADR89630	Adr89630 Human ur1
8	1597	82.2	361	5 ADI16985	Adi16985 Rat NOVX
9	1597	82.2	361	7 ADH69290	Adh69290 Rat orpha
10	1597	82.2	361	8 ADF91782	Adf91782 Rat orpha
11	1597	82.2	361	8 ADR89629	Adr89629 Rat G-pro
12	1597	82.2	361	8 ADS84264	Ads84264 Rat G-pro
13	1561	80.3	361	8 ADO29599	Ado29599 Mouse GPC
14	1127.5	58.0	374	4 AAE04390	Aae04390 Turkey P2
15	1127.5	58.0	374	5 ADI16982	Adi16982 Turkey NO
16	1127.5	58.0	374	8 ADR89631	Adr89631 Turkey G-
17	1007.5	51.8	537	5 AAU74538	Aau74538 Human P2Y
18	1007.5	51.8	537	5 ADI16981	Adi16981 Human NOV
19	1007.5	51.8	537	8 ADR89632	Adr89632 Xenopus p
20	965	49.6	377	4 AAE01144	Aae01144 Human pur
21	965	49.6	377	4 AAE01143	Aae01143 Human pur
22	965	49.6	377	4 AAE04392	Aae04392 Human pur
23	965	49.6	377	6 ABP81866	Abp81866 Human pur
24	965	49.6	377	7 ADE62766	Ade62766 Human Pro

25	965	49.6	377	8 ADO29596	Ado29596 Human GPC
26	965	49.6	377	8 ADP49189	Adp49189 Human P2Y
27	962.5	49.5	373	5 AAE20604	Aae20604 Mus muscu
28	962.5	49.5	373	8 ADO29597	Ado29597 Mouse GPC
29	951	48.9	341	6 ABU63310	Abu63310 Mouse P u
30	950	48.9	374	7 ADE62764	Ade62764 Rat Prote
31	950	48.9	374	8 ADR89633	Adr89633 Rat P20 p
32	928	47.7	375	2 AAR72457	Aar72457 Human P20
33	642.5	33.1	302	8 ADO30396	Ado30396 Mouse GPC
34	641.5	33.0	373	4 AAE04389	Aae04389 Human P2-
35	641.5	33.0	373	5 ABP54316	Abp54316 Human P2Y
36	641.5	33.0	373	5 AAU10983	Aau10983 Purinergi
37	641.5	33.0	373	5 AAU10984	Aau10984 Purinergi
38	641.5	33.0	373	6 ABP81867	Abp81867 Human pur
39	641.5	33.0	373	7 ADD46171	Add46171 Human Pro
40	641.5	33.0	373	8 ADF43210	Adf43210 Human P2R
41	641.5	33.0	373	8 ADO29592	Ado29592 Human GPC
42	641.5	33.0	373	8 ADP49187	Adp49187 Human P2Y
43	641.5	33.0	373	8 ADR89628	Adr89628 Human pur
44	641.5	33.0	373	9 AEA50202	Aea50202 P2RY1. 8/
45	634.5	32.6	373	5 AAU10985	Aau10985 Purinergi

ALIGNMENTS

RESULT 1

AAW23606

ID AAW23606 standard; protein; 365 AA.

AC AAW23606;

XX

DT 31-MAR-1998 (first entry)

XX

DE Human P2Y4 receptor polypeptide.

XX

KW Receptor; P2Y4; pyrimidine binding; uridine triphosphate; UTP.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

FT Domain

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FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Modified-site 345 /note= "potential protein kinase C (PKC) phosphorylation site"

FT Modified-site 359 /note= "potential protein kinase C (PKC) phosphorylation site"

XX WO9719170-A1.

XX 29-MAY-1997.

XX 21-NOV-1996; 96WO-BE000123.

XX 21-NOV-1995; 95EP-00870124.

XX (EURO-) EUROSREEN SA.

XX Communi D, Pirotton S, Parmentier M, Boeynaems J;

XX WPI; 1997-402177/37.

XX N-PSDB; AAT74321.

XX Receptor having preference for pyrimidine over purine nucleotide(s) - especially uridine triphosphate, agonist and antagonists of which are useful in treatment of cystic fibrosis.

XX Claim 1; Fig 1; 56pp; English.

XX This sequence represents a novel human P2 receptor, P2Y4, which has a preference for pyrimidine binding, especially uridine triphosphate. This receptor could be used to screen for novel drugs which specifically bind to it. Transgenic animals could be used to determine the physiological effects of expressing varying levels of the receptor or to identify novel agonists or antagonists. The agonists and antagonists of human P2Y4 may be used, e.g., in treatment of cystic fibrosis

XX Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-203;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTLMWF 60

Db 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTLMWF 60

Qy 61 IFRLPWDATATYMPHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120

Db 61 IFRLPWDATATYMPHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120

Qy 121 CSVLELTCSVHYRIGICHPLEALRWGRPRLAGLCLAVLWVAGCLVPNLFVTTSNKG 180

Db 121 CSVLELTCSVHYRIGICHPLEALRWGRPRLAGLCLAVLWVAGCLVPNLFVTTSNKG 180

Qy 181 TTVLCHDTRPREFHYHFHSAVGMGLFGVCLVTLVCYGLMARLYQPLPGSAQSSSR 240

Db 181 TTVLCHDTRPREFHYHFHSAVGMGLFGVCLVTLVCYGLMARLYQPLPGSAQSSSR 240

Qy 241 LRSLETLAVLVTFVFCVFPFHITRTIYYLARBLEADCKVLNINNVVYKTRPLASNSC 300

Db 241 LRSLETLAVLVTFVFCVFPFHITRTIYYLARBLEADCKVLNINNVVYKTRPLASNSC 300

Qy 301 LDPVLYLTGDKYRQLRQLCGGKQPPRTAASSLALVSLPDESSCRWAATPDSSCSTP 360

Db 301 LDPVLYLTGDKYRQLRQLCGGKQPPRTAASSLALVSLPDESSCRWAATPDSSCSTP 360

Qy 361 RADRL 365

Db 361 RADRL 365

RESULT 2

AAE04391

ID XX AAE04391 standard; protein; 365 AA.

AC XX AAE04391;

XX 04-SEP-2001 (first entry)

DE Human P2Y4 pyrimidinergic receptor.

XX Human; P2-purineric receptor; P2Y1; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrania; eating disorder; depression; angiotensin; peripheral vascular disease; platelet aggregation; restenosis; embolism; thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein; Gi; disseminated intravascular coagulation; P2Y4 pyrimidinergic receptor; thrombosis.

OS Homo sapiens.

XX WO200146454-A1.

XX 28-JUN-2001.

XX 26-DEC-2000; 2000WO-US034998.

XX 23-DEC-1999; 99US-0171622P.

XX (CORT-) COR THERAPEUTICS INC.

XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

XX Hollopeter G;

XX WPI; 2001-418082/44.

XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications.

XX Disclosure; Page 97-98; 108pp; English.

The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purineric receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin-sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombocytopenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrania, eating disorders, depression, migraine and other brain disorders. The present sequence is human P2Y4 pyrimidinergic receptor related to the invention

Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 4; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-203;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTLMWF 60

Db 1 MASTESSLLRSLGSPGSGSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTLMWF 60

Qy 61 IFRLPWDATATYMPHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120

Db 61 IFRLPMDATATYMEHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120
Qy 121 CSVLFLTCISVHYRGLGICHPRLRWGRPRLAGLLCLAVLVVACLVNPLFFVTTNSKG 180
Db 121 CSVLFLTCISVHYRGLGICHPRLRWGRPRLAGLLCLAVLVVACLVNPLFFVTTNSKG 180
Qy 181 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
Db 181 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240
Qy 241 LRSRTIAVLTAVFVAVCFVPHITRTIYLLARLEADCRVLNINVVYKVTPLASANS 300
Db 241 LRSRTIAVLTAVFVAVCFVPHITRTIYLLARLEADCRVLNINVVYKVTPLASANS 300
Qy 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSLALVSLPDSRCRWAATPDSSCSTP 360
Db 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSLALVSLPDSRCRWAATPDSSCSTP 360
Qy 361 RADRL 365
Db 361 RADRL 365

RESULT 3

ABP81923 standard; protein; 365 AA.

AC ABP81923;

XX 04-MAR-2003 (first entry)

XX Human pyrimidinergic receptor P2Y4 protein SEQ ID NO:332.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42771.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G

CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82019, which are used in the
CC exemplification of the present invention
XX
XX Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 6; Length 365;

Best Local Similarity 100.0%; Pred. NO. 1.1e-203; Mismatches 0; Indels 0; Gaps 0;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGSLSPGSGSEVELDCWDFEDFKFILLPVSYAVVFLGLGNAPTLLWF 60

Db 1 MASTESSLLRSLGSLSPGSGSEVELDCWDFEDFKFILLPVSYAVVFLGLGNAPTLLWF 60

Qy 61 IFRLPMDATATYMEHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120

Db 61 IFRLPMDATATYMEHLALSDTLVYLSLPTLIYYAAHNNHWPFGTEICKFVRFYWNLY 120

Qy 121 CSVLFLTCISVHYRGLGICHPRLRWGRPRLAGLLCLAVLVVACLVNPLFFVTTNSKG 180

Db 121 CSVLFLTCISVHYRGLGICHPRLRWGRPRLAGLLCLAVLVVACLVNPLFFVTTNSKG 180

Qy 181 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240

Db 181 TTVLCHDTRPEEFHYVHFSSAVMGLLFGVPCLVTLVYGLMARLYQPLPGSAQSSSR 240

Qy 241 LRSRTIAVLTAVFVAVCFVPHITRTIYLLARLEADCRVLNINVVYKVTPLASANS 300

Db 241 LRSRTIAVLTAVFVAVCFVPHITRTIYLLARLEADCRVLNINVVYKVTPLASANS 300

Qy 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSLALVSLPDSRCRWAATPDSSCSTP 360

Db 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSLALVSLPDSRCRWAATPDSSCSTP 360

Qy 361 RADRL 365

Db 361 RADRL 365

RESULT 4

ADO29598

ID ADO29598 standard; protein; 365 AA.

XX ADO29598;

XX 29-JUL-2004 (first entry)

XX Human GPCR P2RY4, SEQ ID NO:700.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;

kidney disorder; liver disorder; lung disorder; breast disorder;
 ovary disorder; uterus disorder; prostate disorder; testis disorder;
 skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 cycostatic; antinflammatory; vasotropic; antianaginal; antiarrhythmic;
 CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 dermatological; antitumor; antithyroid; antiallergic; anorectic;
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 receptor.

Homo sapiens.

WO2004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

WPI; 2004-390329/36.

DR N-PSDB; ADO30018.

Novel mammalian G protein coupled receptors, useful for identifying
 compounds that modulates diagnosing and treating disease condition
 associated with GPCR dysfunction e.g. autoimmune diseases, angina
 pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 700; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors
 (GPCRs) and nucleic acids encoding them. The invention also relates to
 sequences at least 90% identical to the GPCR proteins and nucleic acids
 of the invention; methods of treating, preventing or diagnosing diseases
 associated with GPCRs of the invention; methods of screening for
 compounds useful in the treatment of GPCR-related diseases; a transgenic
 mouse comprising a GPCR gene of the invention; a mouse comprising a
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 from the transgenic mice; kits comprising several mice, each of which has
 a mutation in a different GPCR gene of the invention; and kits comprising
 probes which hybridise to GPCR polynucleotides of the invention. The
 invention further discloses variants of the GPCR polypeptides and vectors
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 be used in the diagnosis, treatment or prevention of a wide variety of
 diseases including neurological disorders (e.g., Alzheimer's disease,
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 disorders of the adrenal gland; disorders of the colon or intestine
 (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 myocardial infarction); muscular disorders; blood disorders (e.g.,
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 diseases); and disorders of the kidney, liver, lung, breast, ovary,
 uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 thyroid (e.g., cancers). The present sequence represents a GPCR of the
 invention. Note: The full sequence data for this patent did not form part
 of the printed specification; those sequences not shown were obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 8; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.1e-203;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTESLLRSLGSLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLNAPTLLWF 60
 DB 1 MASTESLLRSLGSLSPGSGSEVELDCWDFEDPKFILLPVSYAVVFLGLNAPTLLWF 60

QY 61 IFLRPMWDATATMFMHLSLDTLYVLSLPTLIYYAAHNPFCFTEICKFVRFLFYNNLY 120
 DB 61 IFLRPMWDATATMFMHLSLDTLYVLSLPTLIYYAAHNPFCFTEICKFVRFLFYNNLY 120

QY 121 CSVLFTICISVHYRLGICHPLRALRWRGRPRLAGLLCLAVMLVWAGCLVPLNLFVTTNSKG 180
 DB 121 CSVLFTICISVHYRLGICHPLRALRWRGRPRLAGLLCLAVMLVWAGCLVPLNLFVTTNSKG 180

QY 181 TTVLCHDTTRPEEFDHVHFSSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240
 DB 181 TTVLCHDTTRPEEFDHVHFSSAVMGLLFGVPCLVTLVYGLMARLLYQPLPGSAQSSSR 240

QY 241 LRSRTIAVLTVPVAVCFVPHITRTIYLLARLEADCRVLNIWVYKVTPLASANSC 300
 DB 241 LRSRTIAVLTVPVAVCFVPHITRTIYLLARLEADCRVLNIWVYKVTPLASANSC 300

QY 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSIALVSLPESSCRWAATPDSSCSTP 360
 DB 301 LDPVLYLLTGDKYRRLQRLCGGKQPRTAAASSIALVSLPESSCRWAATPDSSCSTP 360

QY 361 RADRL 365
 DB 361 RADRL 365

RESULT 5
 ADP49193
 ID ADP49193 standard; protein; 365 AA.

XX AC ADP49193;

XX DT 26-AUG-2004 (first entry)

XX DE Human P2Y4 purinergic receptor protein sequence for odour modulation.

XX KW odour sensitivity; P2X purinergic receptor; P2Y purinergic receptor;
 KW signal transduction pathway; olfactory signalling; micro-array.

XX OS Homo sapiens.

XX PN WO2004047749-A2.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-US037389.

XX PR 21-NOV-2002; 2002US-0428140P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PI Lucero M, Hegg C;

XX DR WPI; 2004-460642/43.

XX PT Modulating odor sensitivity in a subject, comprises administering a
 PT composition comprising an agonist or antagonist of P2X or P2Y purinergic
 PT receptor to the subject.

XX PS Disclosure; SEQ ID NO 22; 108pp; English.

XX CC The invention relates to a method of modulating (MI) odour sensitivity in
 CC a subject, by administering a composition which is an agonist or
 CC antagonist of a P2X or P2Y purinergic receptor. (MI) is useful for
 CC modulating odour sensitivity in a subject (claimed). The compositions
 CC used for modulating odour sensitivity in a subject are useful for
 CC studying the signal transduction pathways related to olfactory signaling.
 CC The compositions are also useful as reagents in micro-arrays or as

CC reagents to probe or analyze existing micro-arrays. This sequence
 CC corresponds to the human P2Y4 protein sequence.

XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 8; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-203; Indels 0; Gaps 0;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
 DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
 QY 61 IFRLRPMDATATYMFHALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 120
 DB 61 IFRLRPMDATATYMFHALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 120
 QY 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
 DB 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
 QY 181 TTVLCHDTRTRPEEPDHYHFSSAVMGLLFGVPCLVLCYGLMARRLYQPLPGSAQSSSR 240
 DB 181 TTVLCHDTRTRPEEPDHYHFSSAVMGLLFGVPCLVLCYGLMARRLYQPLPGSAQSSSR 240
 QY 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKTRPLASANS 300
 DB 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKTRPLASANS 300
 QY 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
 DB 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
 QY 361 RADRL 365
 DB 361 RADRL 365

RESULT 6

ADE40463

ID ADE40463 standard; protein; 365 AA.

XX ADE40463;

XX 29-JAN-2004 (first entry)

XX Human pyrimidinergic GPCR P2Y4 (gene ID 326) protein.

XX AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
 KW HIV-related disorder; differential expression; drug screening;
 KW viral replication modulation; diagnosis; prognosis; predisposition;
 KW anti-HIV; gene therapy; antitense therapy; human;
 KW pyrimidinergic GPCR P2Y4; receptor.

XX Homo sapiens.

OS WO2003070883-A2.

XX 28-AUG-2003.

XX 13-FEB-2003; 2003WO-US004246.

XX 15-FEB-2002; 2002US-0357391P.

XX 13-MAY-2002; 2002US-0380249P.

XX 25-JUN-2002; 2002US-0391306P.

XX 27-AUG-2002; 2002US-0462297P.

XX 19-SEP-2002; 2002US-0412007P.

XX 10-OCT-2002; 2002US-0417508P.

XX 10-DEC-2002; 2002US-0432318P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Powell DM, Weich NS;

XX

XX

DR

DR N-PSDB; ADE40462.

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WPI; 2003-671808/63.

N-PSDB; ADE40462.

Identifying a compound capable of diagnosing, preventing or treating AIDS or an HIV-related disorder comprises assaying the ability of the compound to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or polypeptide activity.

Claim 1; SEQ ID NO 42; 167pp; English.

The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus)-related disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADE40422-ADE40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds identified to modulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-related disorders, and for the identification of individuals exhibiting a predisposition to such conditions. The modulatory compounds identified using the method of the invention may be small organic molecules, peptides, antibodies or antisense nucleic acid molecules. The methods of the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.

Sequence 365 AA;

Query Match 99.4%; Score 1932; DB 7; Length 365;

Best Local Similarity 99.2%; Pred. No. 2.3e-202;

Matches 362; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
 DB 1 MASTESSLLRSGLSPGSGSEVELDCWDFDKFILLPVSYAVVFLGLGNAPTLMWF 60
 QY 61 IFRLRPMDATATYMFHALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 120
 DB 61 IFRLRPMDATATYMFHALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 120
 QY 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
 DB 121 CSVLFLTCISVHRYLIGICHPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNFFVTTSNKG 180
 QY 181 TTVLCHDTRTRPEEPDHYHFSSAVMGLLFGVPCLVLCYGLMARRLYQPLPGSAQSSSR 240
 DB 181 TTVLCHDTRTRPEEPDHYHFSSAVMGLLFGVPCLVLCYGLMARRLYQPLPGSAQSSSR 240
 QY 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKTRPLASANS 300
 DB 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKTRPLASANS 300
 QY 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
 DB 301 LDPVLYLLTGDKYRRQLRQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
 QY 361 RADRL 365
 DB 361 RADRL 365

RESULT 7

ADR89630

ID ADR89630 standard; protein; 316 AA.

XX ADR89630;

XX 02-DEC-2004 (first entry)

XX

XX

XX

XX

XX

DE Human uridine nucleotide receptor.
XX HGPBMY23; G-protein coupled receptor; receptor; human;
KW uridine nucleotide receptor.
XX OS
XX Homo sapiens.
XX WO2004076636-A2.
XX
XX 10-SEP-2004.
XX
XX 26-FEB-2004; 2004WO-US005535.
XX
XX 26-FEB-2003; 2003US-00375157.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Barber LE, Cacace A, Feder JN, Nelson TC, Ramanathan CS;
PI Ryseck R, Neubauer MG, Kornacker MG;
XX
XX WPI; 2004-653403/63.
XX SWISSPROT; P51582.
XX
XX New nucleic acid molecules encoding HGPBMY23 polypeptides of the G-
PT protein coupled receptor superfamily, useful for diagnosing, treating, or
PT ameliorating pulmonary, renal, or proliferative disorders, e.g. cancer.
XX
XX Disclosure; SEQ ID NO 10; 370pp; English.
XX
XX The present sequence is that of human uridine nucleotide receptor. The
CC sequence shows 32% identity and 40% similarity to the protein sequence
CC ADR89622 of novel human G-protein coupled receptor HGPBMY23. The
CC invention provides HGPBMY23 polypeptides and polynucleotides, vectors,
CC host cells, antibodies, and recombinant and synthetic methods for
CC producing the polypeptides. Methods are provided for identifying agonists
CC and antagonists of HGPBMY23. The polypeptides, polynucleotides,
CC modulators and methods are useful for diagnosing, treating or
CC ameliorating a disease or disorder related to HGPBMY23, particularly
CC renal diseases and/or disorders, colon cancer, breast cancer, and
CC diseases and disorders related to aberrant NPKappaB modulation.
XX
XX Sequence 316 AA;
SQ
Query Match 85.1%; Score 1653.5; DB 8; Length 316;
Best Local Similarity 86.6%; Pred. No. 6e-172;
Matches 316; Conservative 0; Mismatches 0; Indels 49; Gaps 1;
QY 1 MASTESSLLRSGLSPGSGSEVELDCWDEDEKFIILLPVSAYVFLGLNAPTLWLF 60
DB 1 MASTESSLLRSGLSPGSGSEVELDCWDEDEKFIILLPVSAYVFLGLNAPTLWLF 34
QY 61 IFRLEPDATATYMFHLALSDTLVLSPLTIYYAAHNPFGTEICKFVRLFYWNLY 120
DB 35 -----YVLSPLTIYYAAHNPFGTEICKFVRLFYWNLY 71
QY 121 CSVLFTCTSVHYLGIHPLRALRWGRPLAGLCLAVLWVAGCLVNLFPVTTNSKG 180
DB 72 CSVLFTCTSVHYLGIHPLRALRWGRPLAGLCLAVLWVAGCLVNLFPVTTNSKG 131
QY 181 TTVLCHDTRPEFDHYHVFSSAVMGLFGVPCVLTVCGLMARLYQPLGSAQSSR 240
DB 132 TTVLCHDTRPEFDHYHVFSSAVMGLFGVPCVLTVCGLMARLYQPLGSAQSSR 191
QY 241 LRSRLTIIVLVFAVCFVPHFTRITTYLARLEADCRVLNIVNVYKTRPLASANS 300
DB 192 LRSRLTIIVLVFAVCFVPHFTRITTYLARLEADCRVLNIVNVYKTRPLASANS 251
QY 301 LDPVLYLLTGDKYRRLQQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360
DB 252 LDPVLYLLTGDKYRRLQQLCGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 311
QY 361 RADRL 365
|||||

Db 312 RADRL 316
RESULT 8
ADI16985
ID ADI16985 standard; protein; 361 AA.
XX
XX AC ADI16985;
XX
XX DT 15-APR-2004 (first entry)
XX
XX Rat NOVX protein homologue SeqID 521.
XX
XX rat; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; str.
XX Rattus norvegicus.
XX
XX WO200268649-A2.
XX
XX 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272789P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276769P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296964P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.

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PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX (CURA-) CURAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 521; 1498pp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments of
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 361 AA;
SQ
Query Match 82.2%; Score 1597; DB 5; Length 361;
Best Local Similarity 82.7%; Pred. No. 1.le-165;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;
QY 1 MASTESSLLRSLGLSPGPGSEVLDQWDFDKFILLPVSVYVFLVGLGLNAPTLLWF 60
DB 1 MTSASLLFTSLGSPSSGDG----DCRFNEEFKILLPMYAVVFLVGLGLNAPTLLWF 56
QY 61 IFLRLPMDATATYMFHLASDTLYVLSLPTLYLYYAAHNPFGTEICKFVRFLLFYNNLY 120
DB 57 LFLRLPMDATATYMFHLASDTLYVLSLPTLYLYYAAHNPFGTEICKFVRFLLFYNNLY 116
QY 121 CSQLFLTCISVHRVYLGICHPRLALRWGRPRLAGLLCLAVLWLVAGCLVPLNFFVTTNSKG 180
DB 117 CSQLFLTCISVHRVYLGICHPRLALRWGRPRFASLLCLGWLWLVAGCLVPLNFFVTTNANG 176
QY 181 TTVLCHDTPRPEPDHYHVFSSAVMGLLPVCLVTLVYCYGLMARLLYQPLPGSAQSSSR 240
DB 177 TTILCHDTPLEPDHYHVFSSAVMGLLPVCLVTLVYCYGLMARLLYRPLPGQAQSSSR 236

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QY 241 LRSRTTAVLTVFAVCFVPHITRTIYTLARLLQDCRVLNI VNVVYKVTPLASNSC 300
DB 237 LRSRTTAVLTVFAVCFVPHITRTIYTLARLLQDCRVLNI VNVVYKVTPLASNSC 296
QY 301 LDPVLYLLTGDKYRRLQRLQCGGKQPQRTAASSIALVSLPEDSSCRWAATPQDSSCSTP 360
DB 297 LDPVLYLLTGDKYRRLQRLQCGGKQPQRTAASSIALVSLPEDSSCRWAATPQDSSCSTP 356
QY 361 RADRL 365
DB 357 EGDRL 361
RESULT 9
ADH69290
ID ADH69290 standard; protein; 361 AA.
XX
XX AC ADH69290;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Rat orphan GPCR protein.
XX
XX KW G-protein coupled receptor; GPCR; leukaemia; renal disorder;
KW reproductive disorder; breast cancer; ovarian cancer; uterine cancer;
KW cervical cancer; melanoma; gastrointestinal disorder; colon cancer;
KW multiple myeloma; immune deficiency; B-cell neoplasm; T-cell neoplasm;
KW Hodgkin's disease; follicular lymphoma; splenic marginal zone lymphoma;
KW nodal marginal zone lymphoma; mantle cell lymphoma; hairy cell leukaemia;
KW polymphocytic leukaemia; lymphoplasmacytic lymphoma; Sezary syndrome;
KW smoldering adult T cell leukaemia; Burkitt's lymphoma;
KW post-organ transplant lymphoma; Castleman's disease;
KW Rosai-Dorfman's disease; lymphomatoid papulosis; non-Hodgkin's lymphoma;
KW infection; HIV; human immune deficiency virus; autoimmune disorder;
KW Sjogren's syndrome; gene therapy; cytostatic; antibacterial; virucide;
KW neuroprotective; inotropic; relaxant; gynaecological; gastrointestinal;
KW cardiant; cardiovascular; nephrotropic; hepatotropic; immunostimulant;
KW immunosuppressive; cerebroprotective; vasotropic; nootropic;
KW antiallergic; vulnery; rat.
XX
XX OS Rattus sp.
XX
XX US2003175748-A1.
XX
XX 18-SEP-2003.
XX
XX 10-OCT-2002; 2002US-00268332.
XX
XX 27-SEP-2000; 2000US-0235713P.
XX 16-JAN-2001; 2001US-0261783P.
XX 13-JUL-2001; 2001US-0305085P.
XX 17-AUG-2001; 2001US-0313171P.
XX 26-SEP-2001; 2001US-00964821.
XX
XX (FEDE/) FEDER J N.
XX (MINT/) MINTIER G.
XX (RAMA/) RAMANATHAN C S.
XX (HAWK/) HAWKEN D R.
XX (CACA/) CACACE A.
XX (BARB/) BARBER L E.
XX (KORN/) KORNAKER M G.
XX
XX Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;
XX Barber LE, Kornacker MG;
XX
XX WPI; 2003-898525/82.
XX
XX New isolated nucleic acids encoding G-protein coupled receptor
XX polypeptide, useful for diagnosing, treating, ameliorating and/or
XX preventing disorders, such as cancer, infections, cardiovascular and
XX inflammatory diseases.
XX

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PS Disclosure; SEQ ID NO 15; 90pp; English.

XX The present invention relates to human G-protein coupled receptors (GPCRs), HGP360 and polynucleotides encoding such receptors. The invention is useful for preventing, treating and/or ameliorating an immune disorder, proliferative disorder of the immune system, proliferative disorder of the haematopoietic system, proliferative disorder of B-cells, proliferative disorder of T-cells, proliferative disorder of lymph nodes, proliferative disorder of the spleen, leukaemia, a renal disorder, proliferative disorder of the kidney, reproductive disorder, proliferative disorder of the breast, breast cancer, proliferative disorder of the ovary, ovarian cancer, proliferative disorder of the uterus, uterine cancer, proliferative disorder of the cervix, cervical cancer, proliferative disorder of the skin, melanoma, gastrointestinal disorder, proliferative disorder of the colon, colon cancer, multiple myeloma, immune deficiencies, B-cell neoplasms, T-cell neoplasms, Hodgkin's disease, lymphoma, follicular lymphoma, splenic marginal zone lymphoma, nodal marginal zone lymphoma, mantle cell lymphoma, hairy cell leukaemia, prolymphocytic leukaemia (B cell or T cell), lymphoplasmacytic lymphoma, Sezary syndrome, smoldering adult T cell leukaemia/lymphoma, Burkitt's lymphoma, post-organ transplant lymphoma, Castleman's disease, Rosai-Dorfman's disease, lymphomatoid papulosis, non-Hodgkin's lymphoma, increased susceptibility to HPV infection, increased susceptibility to HIV infection, increased susceptibility to herpes viral infections, increased susceptibility to H. pylori infections, autoimmune disorders, Sjogren's syndrome. The invention is also useful in gene therapy. The present sequence is rat orphan GPCR protein.

XX Sequence 361 AA;

Query Match 82.2%; Score 1597; DB 7; Length 361;
Best Local Similarity 82.7%; Pred. No. 1.1e-165;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 1 MASTESSLLRSLGSPGSSSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTMLWF 60
DB 1 MTSAESLLFTSLGSPSSGSGD-----DCRFNEBFKILLPMSYAVVVLGLGNAPTMLWF 56

QY 61 IFLRLPMDATATYMFHALSDTLVLSLPTLYVYAAHNPFGTEICKVRFLEFYNLY 120
DB 57 LFLRLPMDATATYMFHALSDTLVLSLPTLYVYAAHNPFGTEICKVRFLEFYNLY 116

QY 121 CSVLFTCTSVHRYLGICHLRALRWGRPRLAGLCLAVLVVAGCLVPLNFFVTTSNGK 180
DB 117 CSVLFTCTSVHRYLGICHLRALRWGRPRFASLLCGVLVAGCLVPLNFFVTTSNGK 176

QY 181 TTVLCHDTRPEEDHYHVFSSAVMGLLFGVPLVTLVLCYGLMARRLYQPLGSAQSSSR 240
DB 177 TTVLCHDTRPEEDHYHVFSSAVMGLLFGVPLVTLVLCYGLMARRLYQPLGSAQSSSR 236

QY 241 LRLSLRTIAVLTAVFACVFPFHTRITTYLLALLEADCRVLNVVYKVTPLASANSNC 300
DB 237 LRLSLRTIAVLTAVFACVFPFHTRITTYQARLQADCHLVNVVYKVTPLASANSNC 296

QY 301 LDPVLYLLTGDKYRQLQCGGKQPRTAASSLVSLPDDSSCRWAATPDQSCSTP 360
DB 297 LDPVLYLLTGDKYRQLQCGGKQPRTAASSLVSLPDDSSCRWAATPDQSCSTP 356

QY 361 RADRL 365
DB 357 EGDRL 361

RESULT 10
ADP91782
ID ADP91782 standard; protein; 361 AA.
XX AC ADP91782;
XX DT 26-FEB-2004 (first entry)
XX DE Rat orphan GPCR.

XX KW cytotstatic; anti-HIV; analgesic; anabolic; antiaethma; antiparkinsonian; hypertensive; hypotensive; osteopathic; antiangiatic; cardiant; anti-ulcer; antiallergic; neuroleptic; cardiovascular; neoplastic disease; cancer; tumour; HIV infection; pain; anorexia; intestinal bowel disorder; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; psychotic disorder; immune disorder; metabolic disorder; cardiovascular disorder; neurological disorder; G-protein coupled receptor; HGP360; rat; orphan GPCR.

OS Rattus sp.

XX US2003186360-A1.

XX 02-OCT-2003.

XX 26-SEP-2001; 2001US-00964821.

XX 27-SEP-2000; 2000US-0235713P.

XX 16-JAN-2001; 2001US-0261783P.

XX 13-JUL-2001; 2001US-0305085P.

XX 17-AUG-2001; 2001US-0313171P.

XX (FEDE/) FEDER J N.

XX (MINT/) MINTIER G.

XX (RAMA/) RAMANATHAN C S.

XX (HAWK/) HAWKEN D R.

XX (CACA/) CACACE A.

XX (BARB/) BARBER L.

XX (KORN/) KORNACKER M G.

XX Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A; Barber L, Kornacker MG;

XX WPI, 2004-041196/04.

XX New isolated nucleic acid molecule for treating or preventing, e.g. pain, anorexia, intestinal bowel disorders, bulimia, asthma, or Parkinson's disease.

XX Disclosure; SEQ ID NO 15; 77pp; English.

XX The invention describes an isolated nucleic acid molecule with cytotstatic, anti-HIV, analgesic, anabolic, antiaethma, antiparkinsonian, hypertensive, hypotensive, osteopathic, antiangiatic, cardiant, anti-ulcer, antiallergic, neuroleptic and cardiovascular properties. The invention is used for preventing, treating, or ameliorating a medical condition, e.g. pathological condition. It is used for, e.g. neoplastic diseases such as cancers and tumours, HIV infections, pain, anorexia, intestinal bowel disorders, bulimia, asthma, Parkinson's disease, acute heart failure, hypertension, myocardial infarction, ulcers, allergies, benign prostatic pectoris, myocardial infarction, ulcers, allergies, cardiovascular and hypertrophy, psychotic, immune, metabolic, cardiovascular and neurological disorders. The invention does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues. This is the amino acid sequence of a receptor used in a alignment with the novel human G-protein coupled receptor HGP360 of the invention.

XX Query Match 82.2%; Score 1597; DB 8; Length 361;
Best Local Similarity 82.7%; Pred. No. 1.1e-165;
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 1 MASTESSLLRSLGSPGSSSEVELDCWFDEDFKILLPVSYAVVVLGLGNAPTMLWF 60
DB 1 MTSAESLLFTSLGSPSSGSGD-----DCRFNEBFKILLPMSYAVVVLGLGNAPTMLWF 56

QY 61 IFLRLPMDATATYMFHALSDTLVLSLPTLYVYAAHNPFGTEICKVRFLEFYNLY 120
DB 57 LFLRLPMDATATYMFHALSDTLVLSLPTLYVYAAHNPFGTEICKVRFLEFYNLY 116

QY 121 CSVLFTCTSVHRYLGICHLRALRWGRPRLAGLCLAVLVVAGCLVPLNFFVTTSNGK 180
DB 117 CSVLFTCTSVHRYLGICHLRALRWGRPRFASLLCGVLVAGCLVPLNFFVTTSNGK 176

QY 181 TTVLCHDTRPEEDHYHVFSSAVMGLLFGVPLVTLVLCYGLMARRLYQPLGSAQSSSR 240
DB 177 TTVLCHDTRPEEDHYHVFSSAVMGLLFGVPLVTLVLCYGLMARRLYQPLGSAQSSSR 236

QY 241 LRLSLRTIAVLTAVFACVFPFHTRITTYLLALLEADCRVLNVVYKVTPLASANSNC 300
DB 237 LRLSLRTIAVLTAVFACVFPFHTRITTYQARLQADCHLVNVVYKVTPLASANSNC 296

QY 301 LDPVLYLLTGDKYRQLQCGGKQPRTAASSLVSLPDDSSCRWAATPDQSCSTP 360
DB 297 LDPVLYLLTGDKYRQLQCGGKQPRTAASSLVSLPDDSSCRWAATPDQSCSTP 356

QY 361 RADRL 365
DB 357 EGDRL 361

RESULT 10
ADP91782
ID ADP91782 standard; protein; 361 AA.
XX AC ADP91782;
XX DT 26-FEB-2004 (first entry)
XX DE Rat orphan GPCR.

Db 57 LFLRLPMDATATYMFHLALSDTLVLSLPTLVVYAAARNHWPFGTGLCKFVRLFYWNLY 116
 Qy 121 CSVLFLTCISVHRVYLGICHLPLRALRWGRPRLAGLLCLAVLWVAGCLVPLNLFVTTSNKG 180
 Db 117 CSVLFLTCISVHRVYLGICHLPLRALRWGRPRFASLLCLGVWLVVAGCLVPLNLFVTTNANG 176
 Qy 181 TTVLCHDTRTPPEFDHYHVFSSAVMGLLFGVPLVTVLCYGLMARRLYQPLPGSAQSSSR 240
 Db 177 TTVLCHDTRTPPEFDHYHVFSSAVMGLLFGVPLVTVLCYGLMARRLYQPLPGSAQSSSR 236
 Qy 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKVRPLASANS 300
 Db 237 LRSRTIAVLTVPFVCFVPHITRTIYQARLQADCHVLNINVVYKVRPLASANS 296
 Qy 301 LDPVLYLTGDKYRRLQOLCGGKPOPRTAASSLALVSLPDSRCRWATPODSSCSTP 360
 Db 297 LDPVLYLTGDKYRRLQOLCGGKPKRPTAASSLALVTLHEESISRWDTHQDSTFSAY 356
 Qy 361 RADRL 365
 Db 357 EGDEL 361

RESULT 11

ADR89629
 ID ADR89629 standard; protein; 361 AA.
 AC ADR89629;

02-DEC-2004. (first entry)

Rat G-protein coupled receptor.

HGPRBMV23; G-protein coupled receptor; receptor; rat.

Rattus sp.

WO2004076636-A2.

10-SEP-2004.

26-FEB-2004; 2004WO-US005535.

26-FEB-2003; 2003US-00375157.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Barber LE, Cacace A, Feder JN, Nelson TC, Ramanathan CS;

Ryseck R, Neubauer MG, Kornacker MG;

WPI; 2004-653403/63.

SWISSPROT; O35811.

New nucleic acid molecules encoding HGPRBMV23 polypeptides of the G-
 protein coupled receptor superfamily, useful for diagnosing, treating, or
 ameliorating pulmonary, renal, or proliferative disorders, e.g. cancer.

Disclosure; SEQ ID NO 9; 370pp; English.

The present sequence is that of a rat G-protein coupled receptor that
 shows 31% identity and 41% similarity to the protein sequence ADR89622 of
 novel human G-protein coupled receptor HGPRBMV23. The invention provides
 HGPRBMV23 polypeptides and polynucleotides, vectors, host cells,
 antibodies, and recombinant and synthetic methods for producing the
 polypeptides. Methods are provided for identifying agonists and
 antagonists of HGPRBMV23. The polypeptides, polynucleotides, modulators
 and methods are useful for diagnosing, treating or ameliorating a disease
 or disorder related to HGPRBMV23, particularly renal diseases and/or
 disorders, colon cancer, breast cancer, and diseases and disorders
 related to aberrant NFkappaB modulation.

Sequence 361 AA;

Query Match 82.2%; Score 1597; DB 8; Length 361;
 Best Local Similarity 82.7%; Pred. No. 1.1e-165;
 Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

Qy 1 MASTESSLLRSLGSLSPGSGSEVELDCWFDKFIPLPVSYAVVVLGLGALNAPTLMWF 60
 Db 1 MTSAESLLFTSLGSPSGSDG---DCRFNEEPKFIPLPMSYAVVVLGLGALNAPTLMWF 56
 Qy 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLVVYAAARNHWPFGTEICKFVRLFYWNLY 120
 Db 57 LFLRLPMDATATYMFHLALSDTLVLSLPTLVVYAAARNHWPFGTGLCKFVRLFYWNLY 116
 Qy 121 CSVLFLTCISVHRVYLGICHLPLRALRWGRPRFASLLCLGVWLVVAGCLVPLNLFVTTSNKG 180
 Db 117 CSVLFLTCISVHRVYLGICHLPLRALRWGRPRFASLLCLGVWLVVAGCLVPLNLFVTTNANG 176
 Qy 181 TTVLCHDTRTPPEFDHYHVFSSAVMGLLFGVPLVTVLCYGLMARRLYQPLPGSAQSSSR 240
 Db 177 TTVLCHDTRTPPEFDHYHVFSSAVMGLLFGVPLVTVLCYGLMARRLYQPLPGSAQSSSR 236
 Qy 241 LRSRTIAVLTVPFVCFVPHITRTIYLLARLEADCRVLNINVVYKVRPLASANS 300
 Db 237 LRSRTIAVLTVPFVCFVPHITRTIYQARLQADCHVLNINVVYKVRPLASANS 296
 Qy 301 LDPVLYLTGDKYRRLQOLCGGKPOPRTAASSLALVSLPDSRCRWATPODSSCSTP 360
 Db 297 LDPVLYLTGDKYRRLQOLCGGKPKRPTAASSLALVTLHEESISRWDTHQDSTFSAY 356
 Qy 361 RADRL 365
 Db 357 EGDEL 361

RESULT 12

ADS84264
 ID ADS84264 standard; protein; 361 AA.
 AC ADS84264;

13-JAN-2005 (first entry)

Rat G protein-coupled receptor O35811.

Rat; receptor; G protein-coupled receptor; GPCR; HGPRBMV3; HGPRBMV11;
 HGPRBMV23; GPCR P210; proliferative disorder; immunological disorder;
 immunodeficiency disease; immune reaction; transplanted rejection;
 autoimmunity disorder; hypersensitivity; cancer; neurological disorder;
 dyskinesia; infection; arthritis; rheumatoid arthritis; asthma;
 leukaemia; granulomatous disease; inflammatory bowel disease; sepsis;
 allergy; acne; neutropenia; psoriasis; AIDS.

Rattus sp.

US2004209808-A1.

21-OCT-2004.

10-FEB-2004; 2004US-00775965.

11-FEB-2003; 2003US-0446655P.

(KORN/) KORNACKER M G.

Kornacker MG;

WPI; 2004-747284/73.

New isolated peptide, useful for treating e.g., immunodeficiency
 diseases, immune reactions to transplanted organs and tissues,
 autoimmunity disorders, hypersensitivities, or proliferative disorders
 (e.g., cancer).

Example 1; SEQ ID NO 15; 113pp; English.

The invention relates an isolated peptide which binds to the human G protein-coupled receptor (GPCR) HGPBRBM3 or to HGPBRBM11, HGPBRMY23 or GPCR P2Y10. Also included are an isolated nucleic acid encoding the peptides, a vector comprising the nucleic acid, a host cell comprising the vector (where the host cell is selected from bacterial, yeast, insect, mammalian, and plant cells), a primer or probe designed against the nucleic acids, a polypeptide complex (comprising a P2Y-type G-protein coupled receptor, and a peptide comprising an amino acid sequence above, or a polypeptide complex comprising a G-protein coupled receptor selected from P2Y10, human G-protein coupled receptor (HGPBRBM3, HGPBRBM11, and HGPBRMY23, and a peptide comprising the amino acid sequence above), an antibody that binds to the peptide, a peptide library generated from the nucleic acid molecules, identifying a binding agent for a P2Y-type G-protein coupled receptor (or G-protein coupled receptor selected from P2Y10, HGPBRBM3, HGPBRBM11, and HGPBRMY23), identifying a P2Y-type G-protein coupled receptor, identifying a binding agent for a P2Y-type G-protein coupled receptor, a kit for detecting a P2Y-type G-protein coupled receptor (comprising the binding peptide or the antibody and one or more reagents for detecting binding of the receptor and the peptide or antibody), diagnosing a proliferative disorder and a pharmaceutical composition (comprising the nucleic acid molecule, the isolated vector, the peptide or the antibody, and a carrier, excipient, or diluent). The pharmaceutical composition is useful for treating a proliferative disorder. The peptides are useful as diagnostic, prophylactic, and therapeutic agents for immunological disorders, immunodeficiency diseases, immune reactions to transplanted organs and tissues, autoimmunity disorders, hypersensitivities, cancer, neurological disorders, dyskinesias, and infection susceptibility, arthritis, rheumatoid arthritis, asthma, leukaemia, granulomatous disease, inflammatory bowel disease, sepsis, allergies, acne, neuropenia, psoriasis, AIDS and many more diseases and disorders given in the specification. The present sequence represents a GPCR homologous to HGPBRBM3.

Sequence 361 AA;

[illegible]

CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 361 AA;

Query Match 80.3%; Score 1561; DB 8; Length 361;
 Best Local Similarity 80.8%; Pred. No. 9.6e-162;
 Matches 295; Conservative 20; Mismatches 46; Indels 4; Gaps 1;
 QY 1 MASTESLLRSGLSPGSGSSEVELDCWDEKFIPLPVSYAVVFLGVLNAPTLLWLF 60
 Db 1 MTSADSLFTSLGSPSSGSGD-----DCKFNEEFKFIPLPVSYAVVFLGVLNAPTLLWLF 56
 QY 61 IFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 120
 Db 57 LFLRLPMDATATYMFHLALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWNLY 116
 QY 121 CSVLFTCTSVHRYLGICHPRLRWGRPRLAGLCLAVLVVAGCLVPLNLPFVTTNKG 180
 Db 117 CSVLFTCTSVHRYLGICHPRLRWGRPRFAGLCLGVVLVAGCLVPLNLPFVTTNANG 176
 QY 181 TTVLCHDTRPEEDHYHVFSSAVMGLLGVPCVCLTVLCYGLMARLYPLPGSAQSSR 240
 Db 177 TTVLCHDTRPEEDHYHVFSSAVMGLLGVPCVCLTVLCYGLMARLYPLPGSAQSSR 236
 QY 241 LRSRLTIIVLVTVFAVCFVPHFTHITRIYYLARLEADCRVLNVVYKTRPLASNSC 300
 Db 237 LRSRLTIIVLVTVFAVCFVPHFTHITRIYYLARLEADCRVLNVVYKTRPLASNSC 296
 QY 301 LDPVLYLLTGDYKVRQLQCGGKQPQRTAASSLALVSLPEDSSCRWAATPDSSCSSTP 360
 Db 297 LDPVLYLLTGDYKVRQLQCGGKQPQRTAASSLALVSLPEDSSCRWAATPDSSCSSTP 356
 QY 361 RADRL 365
 Db 357 EGDRL 361

RESULT 14

AAE04390
 ID AAE04390 standard; protein; 374 AA.

XX AAE04390;

XX 04-SEP-2001 (first entry)

XX Turkey P2Y nucleotide receptor.

XX Turkey; P2-purinergic receptor; P2Y12; vasotropic; thrombolytic;
 KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
 KW myocardial infarction; ischaemic attack; preclampsia; bleeding disorder;
 KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;
 KW peripheral vascular disease; platelet aggregation; restenosis; embolism;
 KW thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
 KW Gi; disseminated intravascular coagulation; P2Y nucleotide receptor;
 KW cardiant; thrombosis.

XX Meleagris gallopavo.

OS WO200146454-A1.

XX 28-JUN-2001.

XX 26-DEC-2000; 2000WO-US034998.

XX 23-DEC-1999; 99US-0171622P.

PA (CORT-) COR THERAPEUTICS INC.

PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Hollopeter G;

XX WPI; 2001-418082/44.

XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 PT for identifying binding partners and for diagnostic applications.

XX Disclosure; Page 95-96; 108pp; English.

XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin-
 CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor
 CC that responds to ADP. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischaemic
 CC attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic and
 CC restenotic complications following angioplasty, carotid endarterectomy,
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
 CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizophrenia, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is turkey P2Y nucleotide
 CC receptor related to the invention

XX Sequence 374 AA;

Query Match 58.0%; Score 1127.5; DB 4; Length 374;

Best Local Similarity 59.3%; Pred. No. 3e-114;

Matches 208; Conservative 56; Mismatches 70; Indels 17; Gaps 4;

QY 9 LRSGLSP-----GPGSSEVELDCWDEKFIPLPVSYAVVFLGVLNAPTLLW 58

Db 5 VRMFLAPWTPTTPWLGNTTAAAEAKCVNEEFKFIPLPVSYAVVFLGVLNAPTLLW 64

QY 59 LFIPLRPMDATATYMFHLALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWN 118

Db 65 IFVSRMRPNWNTTTFMFLALSDTLVLSLPTLIYYAAHNPFGTEICKFVRFYWN 124

QY 119 LYCSVLFTCTSVHRYLGICHPRLRWGRPRLAGLCLAVLVVAGCLVPLNLPFVTTN 178

Db 125 LYSSLFTCTSVHRYLGICHPRLRWGRPRLAGLCLAVLVVAGCLVPLNLPFVTTN 184

QY 179 KGTVLCHDTRPEEDHYHVFSSAVMGLLGVPCVCLTVLCYGLMARLYPLPGSA 235

Db 185 KDNSTLCHDTRPEEDHYHVFSSAVMGLLGVPCVCLTVLCYGLMARLYPLPGSA 244

QY 236 QSSRLSLRTIIVLVTVFAVCFVPHFTHITRIYYLARLEADCRVLNVVYKTRPLA 295

Db 245 VPSYKGSIKMIILVTVFAVCFVPHFTHITRIYYLARLEADCRVLNVVYKTRPLA 304

QY 296 SANSCLDPVLYLLTGDYKVRQLQCGGKQPQRTAASS-LALVSLPEDSS 345

Db 305 SINSCLDPVLYLLTGDYKVRQLQCGGKQPQRTAASS-LALVSLPEDSS 352

RESULT 15

ADI16982
 ID ADI16982 standard; protein; 374 AA.

XX ADI16982;

XX 15-APR-2004 (first entry)

DE Turkey NOVX protein homologue SeqID 518.
 XX turkey; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (IgA) nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; str.

PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
 PI Li L, Gangolli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
 PI Gerlach VL, Taupier RJ, Gusev VI, Colman SD, Wolenc AR, Pena CBA;
 XX Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 DR WPI; 2002-706998/76.
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Disclosure; SEQ ID NO 518; 1498pp; English.

XX This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments of
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, viricide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.
 XX Sequence 374 AA;
 SQ

Query Match 58.0%; Score 1127.5; DB 5; Length 374;
 Best Local Similarity 59.3%; Pred. NO. 38-114;
 Matches 208; Conservative 56; Mismatches 70; Indels 17; Gaps 4;
 QY 9 LRSGLSP-----GPGSSEVLCDFEDEFKILLPVSYAVFVGLGNAPTLW 58
 DB 5 VNFSLAPWPTPTPWLGGNTTAAAEKCVFEEFKILLPIYSGIVFVGLPLNSWAMW 64
 QY 59 LFIFRLRPMDATATYMFHALSDTLVLSLPTLIYYAAHNNHWPFGTECKVRFPLFYNN 118
 DB 65 IFVSRMRPNWNTTYMFLAISDTLVVSLPTLVVYADRNWNPFGKVFCKIVRFLFYAN 124
 QY 119 LYCSVLFLTCISVHRYLGTCHPLRALWGRPRLAGLCLAVNLVAVGLNPNLFFVTTSN 178
 DB 125 LYSSILFLTCISVHRYMGICHPIRSLKWKVKTHARLICVGLWLVVITICLPNLIFFVTTSS 184
 QY 179 KGTTLVCHDTTPEEDFHYVHFSSAVMGLLFGVPCILVTLVLCYGLMARRLYQ---PLFGSA 235
 DB 185 KNSITLCHDTTPEEDFHYVHFSSSIMALLFGIPFLVIVVVCYCLMAKRLCKRSPSPSPR 244
 QY 236 QSSRLRSRTIAVLTFAVCFVPHITRTIYLLARLEADCRVLNIVNVVVKVTRPLA 295
 DB 245 VPSYKRSIKMIIIVLTFAICFVPHITRTIYLLARLEADCRVLNIVNVVVKVTRPLA 304
 QY 296 SANSCLDPVLYLLTGDYKVERQLCGGKGPQPRTRASS-LALVSLPESS 345
 DB 305 SINSCLDPILYFMAGDKYRGLRR---GAAQRPRFVPTSLALVSPVSDSS 352

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(CURA-) CURAGEN CORP.

